

FIG. 1A

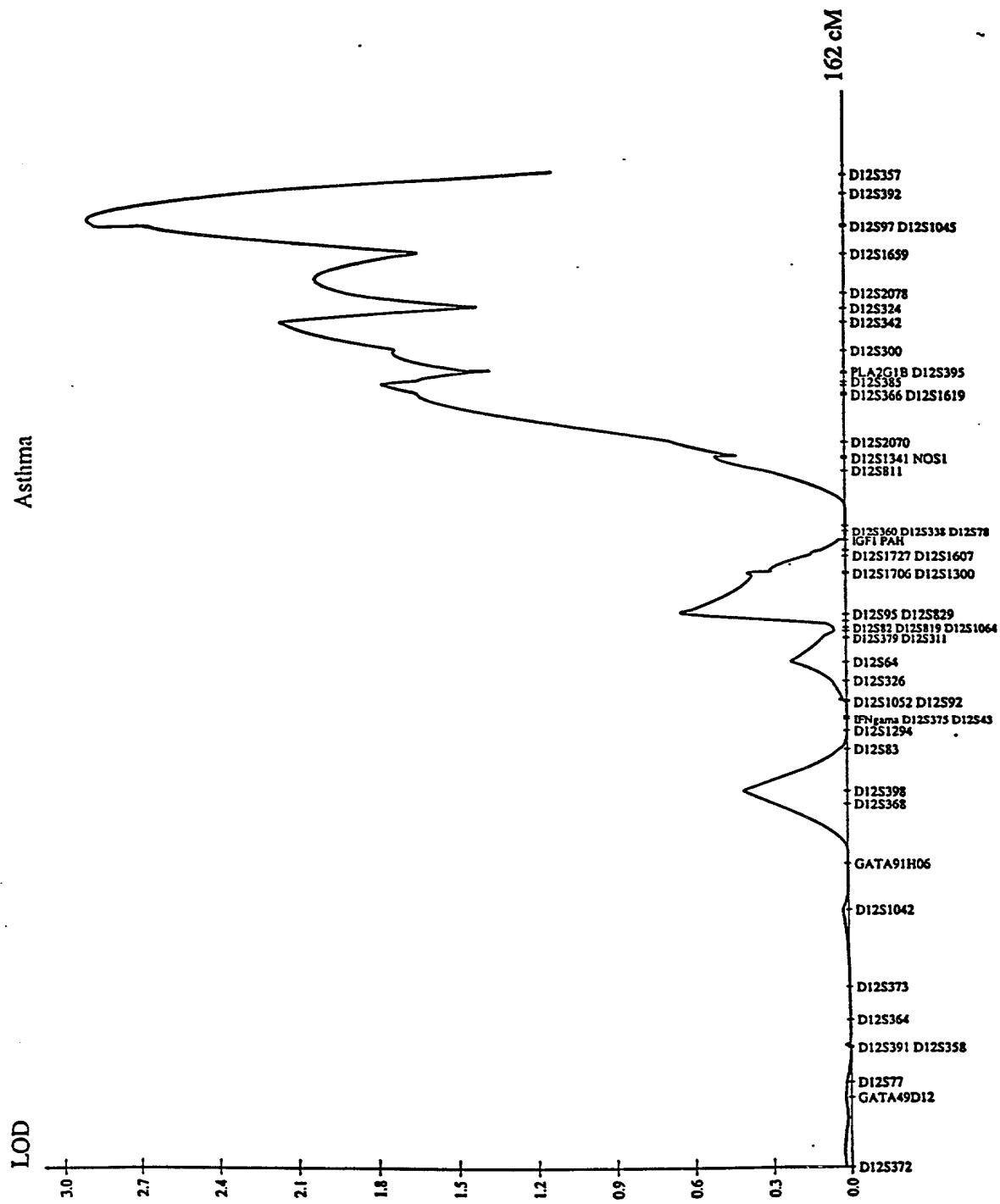
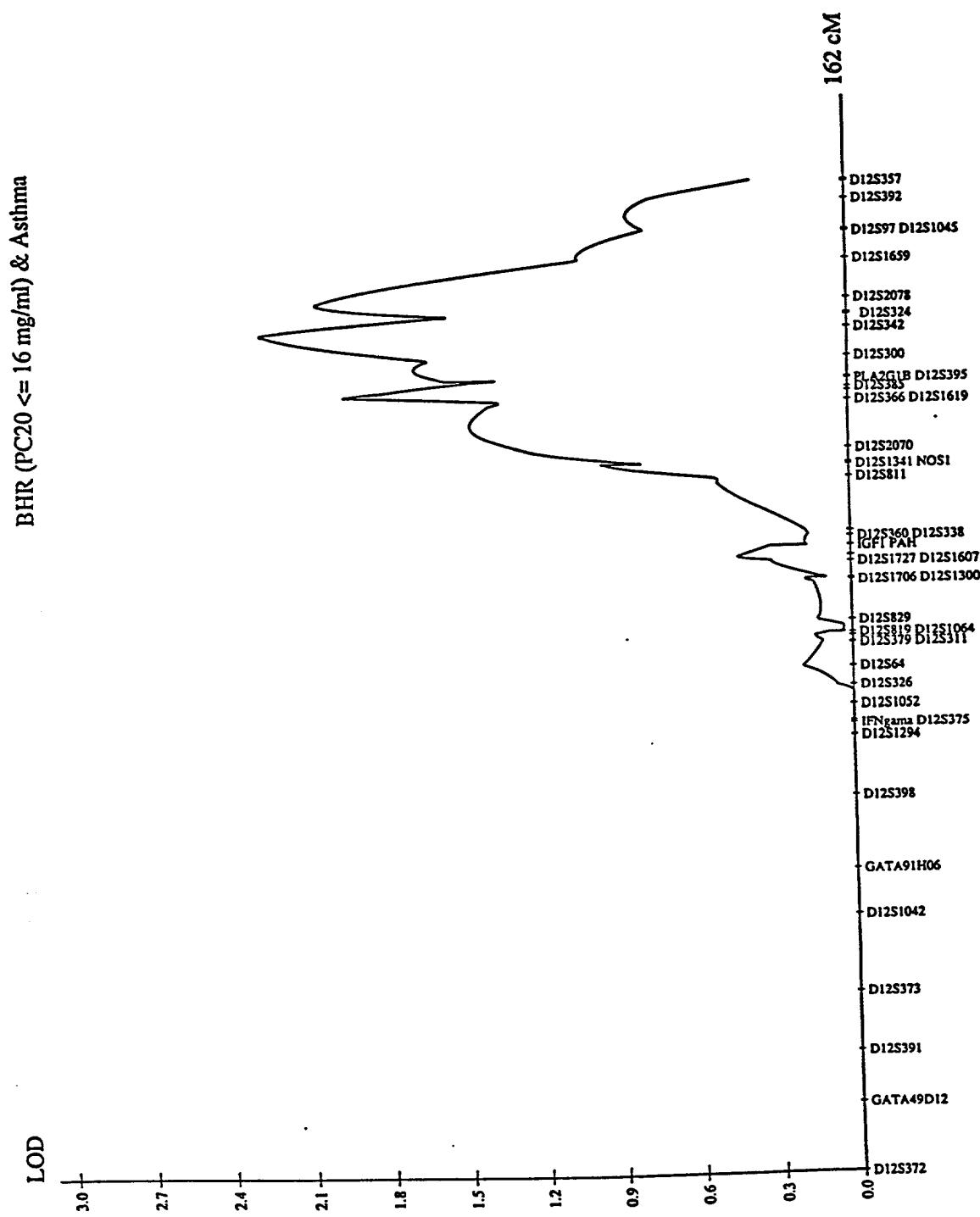


FIG. 1B



High Total IgE & Asthma

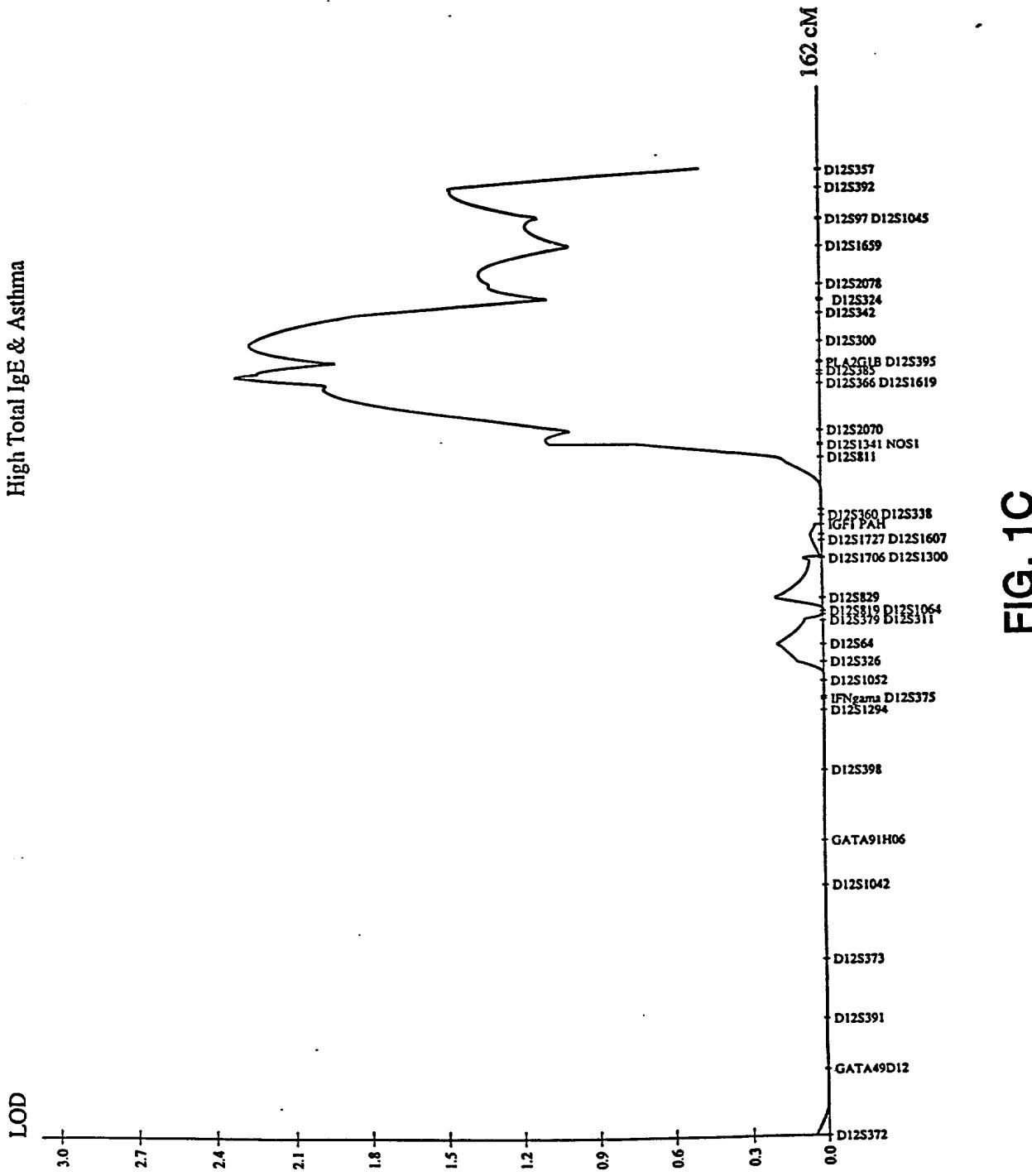
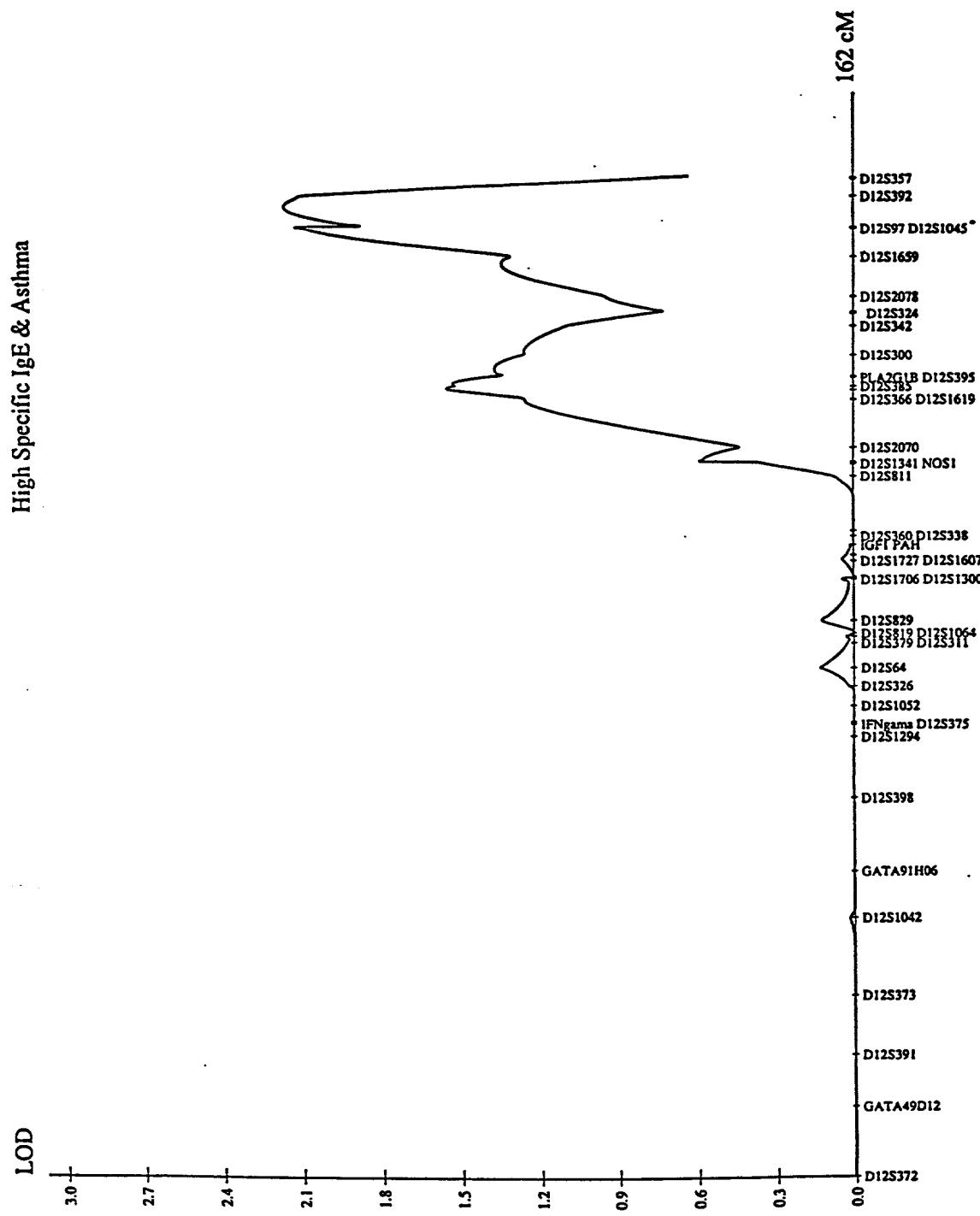
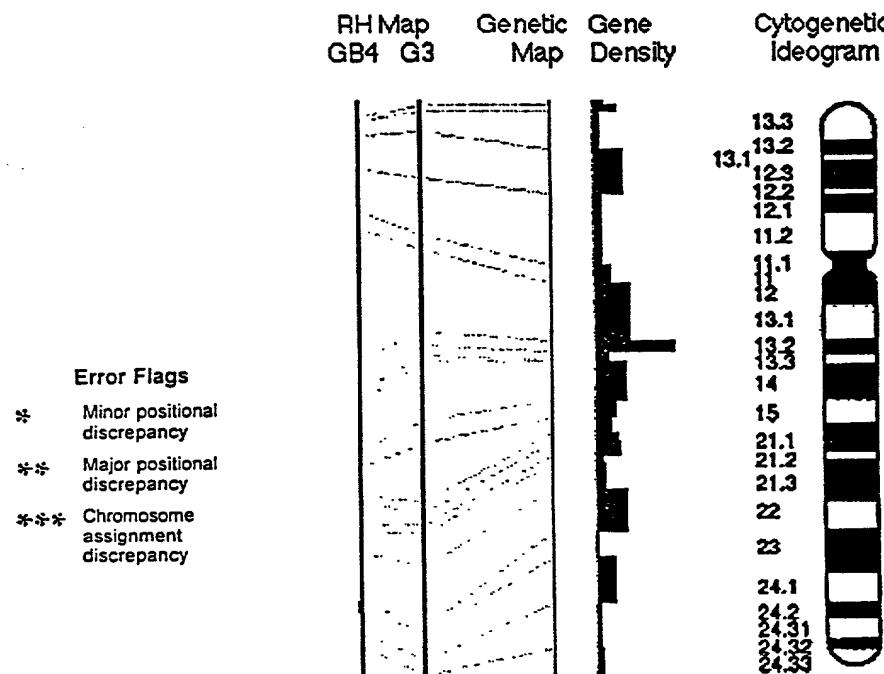


FIG. 1C

FIG. 1D



Chromosome 12: D12S79-D12S366



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S79 (126.1 cM)

Bottom of interval: D12S366 (133.8 cM)

Genetic size of bin: 8 cM

Physical size of bin: 9 cR3000

FIG. 2 A

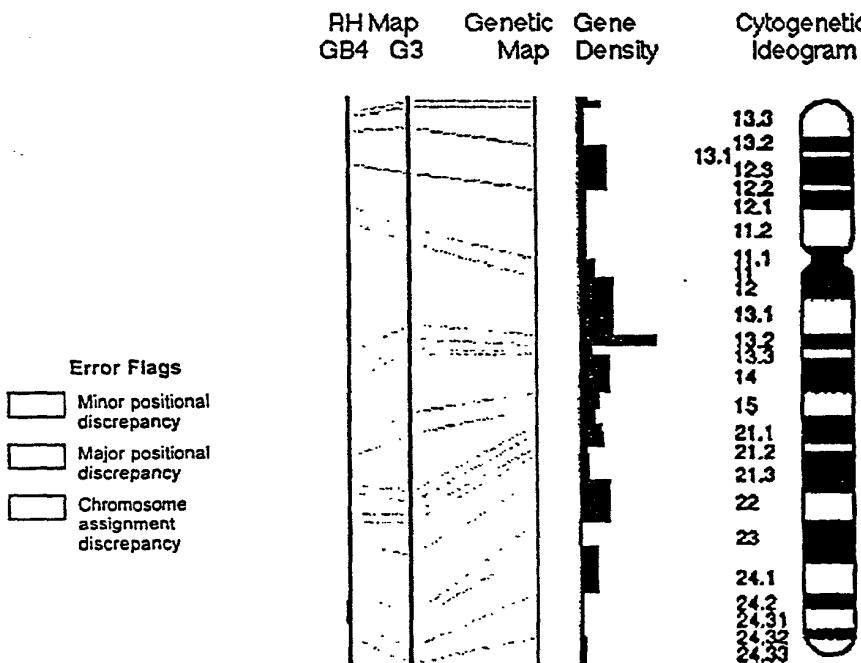
Next interval up

126.1	◆ 451.62 F	AFM067yc5	D12S79	Microsatellite anchor marker AFM067yc5
	454.24 P0.10	A009F32	KIAA0331	KIAA0331 gene product
	455.39 P0.37	sts-N33343		ESTs
	455.39 P1.15	SGC38179		ESTs
	455.70 P0.06	stSG54526		ESTs
	455.81 P1.35	stSG1522		ESTs
	455.86 P2.06	sts-T56610		Homo sapiens mRNA for KIAA0875 protein, p..
	456.02 P2.38	sts-R33659		EST
	456.34 P0.23	sts-D29101		EST
	456.34 P0.04 *	SGC44506		ESTs
	456.86 P2.34	NIB1804		ESTs
	456.86 P>3.00	stSG44263		ESTs, Weakly similar to calcium-binding pr..
	456.86 "	stSG62560		Homo sapiens clone 24852 mRNA sequence
	456.96 P1.66 *	sts-AA001615		ESTs
	456.96 P0.04	sts-T94297		ESTs, Weakly similar to TBX2 gene [H.sapi..
	457.17 P1.31	stSG54365		ESTs
	457.17 P0.13	WI-21497		Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.30	WI-20357		Homo sapiens mRNA for KIAA0875 protein, p..
	457.17 P0.38	SGC31491	NOS1	nitric oxide synthase 1 (neuronal)
	457.17 P0.31	RK903_904	NOS1	nitric oxide synthase 1 (neuronal)
	457.17 P0.18	sts-AA007571		ESTs
	457.17 P1.35	stSG46223		ESTs
	457.17 "	stSG58387		ESTs
◆ 457.27 P>3.00 *	Cdalce05			Homo sapiens clone 23714 mRNA sequence
457.27 P0.10 *	sts-W79390	NME2		non-metastatic cells 2, protein (NM23B) exp..
457.48 P0.20	sts-Z40829			ESTs
460.94 P0.00 *	A005Q47			ESTs
◆ 460.94 F	AFM351tb9	D12S366		Microsatellite anchor marker AFM351tb9

Next interval down

FIG. 2 B

Chromosome 12: D12S366-D12S340



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

Physical size of bin: 21 cR3000

133.8	◆ 460.94 F	AFM351tb9	D12S366	Microsatellite anchor marker AFM351tb9
	462.85 P1.00 *	stSG8109		ESTs
	462.85 "	sts-X75252	PBP	prostatic binding protein
	462.95 P1.04	sts-AA011374		Homo sapiens KIAA0431 mRNA, partial cds

FIG. 2 C

463.77 P0.19	WI-16745		Human clone 37, 5cM region surrounding hepa..
◆ 463.77 P0.20	SGC33949	KIAA0262	KIAA0262 gene product
463.98 P0.02	A008B04		ESTs
463.98 "	stSG50309		ESTs
463.98 "	stSG49970		Homo sapiens mRNA for KIAA0875 protein, p..
463.98 P0.04	stSG27318		Human clone 23932 mRNA sequence
463.98 P0.08	R06295		EST
463.98 P1.33	sts-W56792		ESTs
464.08 P2.32	A007E48		ESTs
464.19 P1.28	A009U43		ESTs
464.29 P1.33	stSG3138		Homo sapiens mRNA for KIAA0949 protein, p..
464.39 P1.09	sts-F21636		Human DNA sequence from BAC 15E1 on chrom..
464.39 P1.13	stSG15685	KIAA0262	KIAA0262 gene product
464.39 "	RP_P0_1	RPLP0	Ribosomal protein large, P0
464.39 P1.09	stSG29626		ESTs
464.39 P1.14	stSG31407		Human DNA sequence from BAC 15E1 on chrom..
464.39 "	A001T32	PXN	paxillin
464.39 "	A001W18		H.sapiens mRNA for AMP-activated protein ..
464.39 "	WIAF-40		Human mRNA for KIAA0219 gene, partial cds
464.39 "	sts-T95105		ESTs
464.39 "	Cda0id01		ESTs
464.39 P1.13	stSG31431		ESTs, Moderately similar to (defline not a..
◆ 464.39 " *	WI-13177		Homo sapiens clone 23714 mRNA sequence
464.39 "	IB1092		Homo sapiens clone 23714 mRNA sequence
464.39 "	T79466		ESTs
464.39 P1.18	stSG48379		ESTs
464.45 P1.05	KIAA0219		Human mRNA for KIAA0219 gene, partial cds
464.45 "	stSG40392		ESTs
464.45 "	stSG31586		H.sapiens mRNA for AMP-activated protein ..
◆ 464.49 P0.21	A006F12	KIAA0152	KIAA0152 gene product
464.49 P0.25	sts-AA002185	PXN	paxillin
464.49 P0.10	stSG48442		ESTs
464.49 "	sts-T16456		ESTs
464.49 "	stSG62260		ESTs

FIG. 2 D

	464.49 "	NIB1331		ESTs
	464.49 "	WI-15518		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	WIAF-1058		ESTs, Moderately similar to unknown [H.sap..
	464.49 "	SGC34758		ESTs
	464.49 "	WI-19738		Homo sapiens mRNA for KIAA0787 protein, p..
	464.49 "	IB383		ESTs, Weakly similar to fos39554 1 [H.sapi..
	464.49 "	SGC32343		ESTs
	464.79 P0.96	SGC33521		ESTs
	464.79 P0.96 *	X58965	NME2	non-metastatic cells 2, protein (NM23B) exp..
	465.20 P0.20	sts-H10302		ESTs
◆	465.38 P0.85	A007E11	KIAA0262	KIAA0262 gene product
	465.41 P0.81	A007I44	RPLP0	ribosomal protein, large, P0
	465.41 "	stSG22726		EST
	465.41 "	WI-17776		ESTs
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 "	stSG31753		Human mRNA for KIAA0219 gene, partial cds
	465.41 P0.77	stSG4775	SFRS9	splicing factor, arginine/serine-rich 9
	465.41 "	A002J47		ESTs, Weakly similar to heat shock protein..
	465.41 P0.80	stSG46660		EST
	465.51 P0.75	stSG41086	PXN	paxillin
	465.51 P0.83	stSG52121		ESTs
	465.91 P0.01	WI-16071		ESTs
	465.91 P0.00	WI-13962		H.sapiens mRNA for AMP-activated protein ..
	466.62 P0.00	sts-AA011220	SFRS9	splicing factor, arginine/serine-rich 9
	466.71 P0.00	stSG4712		ESTs, Weakly similar to homology with o251..
	466.91 P0.01	WI-15135		Homo sapiens mRNA for KIAA0787 protein, p..
	466.91 P0.01	D12S2088	TCF1	transcription factor 1, hepatic; LF-B1, hep..
	467.01 P0.01	stSG52567		ESTs
135.1	467.11 F	AFM123xh2	D12S86	Microsatellite marker AFM123xh2
135.1	467.11 P0.01	AFM299zd5	D12S349	Microsatellite marker AFM299zd5
	467.11 P0.01	AFM123xh2		Unknown
137.5	◆ 467.21 P0.02	AFM220zf4	D12S321	Microsatellite marker AFM220zf4
	467.21 P0.02	sts-W73277	SFRS9	splicing factor, arginine/serine-rich 9
	467.21 P0.02	stSG8721		EST

FIG. 2 E

467.21 "	stSG44224		ESTs
467.21 "	stSG49978		H.sapiens mRNA for AMP-activated protein ..
◆ 467.21 "	stSG31862		Homo sapiens HSPC004 mRNA, complete cds
467.21 "	stSG47820		ESTs
467.21 "	Bdac4h06	KIAA0262	KIAA0262 gene product
467.21 "	stSG15021		ESTs
467.21 "	A002B13	SFRS9	splicing factor, arginine/serine-rich 9
◆ 467.21 "	H50549	KIAA0262	KIAA0262 gene product
467.21 P0.03	SGC35167		EST
467.21 P0.03	WI-19637		H.sapiens mRNA for AMP-activated protein ..
467.21 P0.02	WIAF-607		Unknown
467.31 P0.02	WI-16997	RPLP0	ribosomal protein, large, P0
468.93 P0.85	SGC31344		EST
469.13 P0.90	A007C39	ACADS	acyl-Coenzyme A dehydrogenase, C-2 to C-3 ..
469.13 P0.14	stSG35104		ESTs
469.13 "	A006Q41		Unknown
469.23 P0.18	sts-Y07684	P2RX4	purinergic receptor P2X, ligand-gated ion c..
469.33 P0.93	stSG8506		ESTs, Moderately similar to unknown [H.sap..]
469.33 "	R01708		EST
469.33 "	stSG54819	HCALB_BR	calbrain
469.33 "	A001Z45		ESTs, Highly similar to (defline not avail..)
469.33 "	stSG35318		ESTs, Weakly similar to fos39554 1 [H.sapi..]
469.33 "	stSG63173		EST
469.33 "	stSG31374	OASL	2'-5'oligoadenylate synthetase-like
469.42 P1.01	WI-16068		EST
469.44 P0.23	stSG1961		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62627		EST
469.44 "	stSG36007		Homo sapiens full length insert cDNA clone..
469.44 "	stSG39281	P2RX7	purinergic receptor P2X, ligand-gated ion c..
469.44 "	stSG2554		Homo sapiens mRNA for KIAA0787 protein, p..
469.44 "	stSG62591		ESTs
◆ 469.54 P1.03	A006N38	KIAA0152	KIAA0152 gene product
469.62 P1.03	sts-N34573		ESTs
469.62 P1.03	sts-N58045		ESTs

FIG. 2 F

469.62 P1.04	WI-13224		EST
469.83 P1.12	SGC34424		ESTs
469.93 P1.14	stSG3875	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.14 P1.17	stSG52516		ESTs, Weakly similar to (defline not avail..
470.24 P1.32	D0S1735E		ESTs
470.24 P1.12	WI-6178		ESTs
470.32 P1.25	sts-U29895		Unknown
470.32 P1.24	WI-19611	PSMD9	proteasome (prosome, macropain) 26S subunit..
470.43 P1.29	stSG52094		ESTs
470.63 P1.38	A004O17		ESTs
◆ 470.77 P1.32	** SGC33451		ESTs, Weakly similar to rhoHP1 [H.sapiens..
◆ 470.84 P1.35	** sts-X64838	RSN	restin (Reed-Steinberg cell-expressed inter..
470.84 P1.52	WI-13062		Homo sapiens mRNA, expressed in fibroblast..
471.27 P1.60	sts-R99269		EST
471.37 P1.70	stSG1991		ESTs
471.37 "	stSG15859		Homo sapiens full length insert cDNA YQ02..
471.58 P1.78	stSG29729		ESTs, Weakly similar to (defline not avail..
471.58 P1.37	WI-16979		ESTs
471.65 P1.39	WI-17693		EST
471.80 P1.29	WI-22060		ESTs
471.90 P>3.00	stSG8210		ESTs, Moderately similar to neuronal threa..
471.90 "	WI-17956		EST
471.90 "	WI-20969		Homo sapiens mRNA for KIAA0867 protein, c..
471.90 "	stSG47029		ESTs
471.90 "	stSG47647		EST
471.90 "	sts-W45376		Homo sapiens mRNA for KIAA0867 protein, c..
◆ 471.90 "	** WI-6021	RSN	restin (Reed-Steinberg cell-expressed inter..
471.90 "	NIB962		ESTs
471.90 "	A009E34		ESTs, Moderately similar to neuronal threa..
471.90 "	sts-T17477		ESTs
472.08 P1.49	sts-X89984		H.sapiens mRNA for BCL7A protein
472.12 P>3.00	SGC34693		EST
472.12 P>3.00	A009O01		ESTs, Weakly similar to neuronal thread pr..
472.29 P>3.00	stSG47084		ESTs

FIG. 2 G

472.40 P>3.00	stSG58209	EEF1D	eukaryotic translation elongation factor 1 d..
472.40 P>3.00	AA213821	EEF1D	eukaryotic translation elongation factor 1 d..
472.61 P>3.00	A002R44		Unknown
472.61 P>3.00	SGC35850	EEF1D	eukaryotic translation elongation factor 1 d..
472.72 P0.01	sts-H98108		ESTs
472.97 P>3.00	WI-6239		ESTs
473.04 P>3.00	sts-H75490		ESTs
◆ 473.58 P>3.00 **	WI-14983	RSN	restin (Reed-Steinberg cell-expressed inter..
474.01 P>3.00	stSG8610		ESTs
474.01 P>3.00	stSG47080		ESTs
474.38 P2.18	stSG8686		ESTs, Weakly similar to similar to pre-mRN..
474.38 P2.25	stSG26358		ESTs, Weakly similar to similar to pre-mRN..
474.38 "	stSG29931		ESTs
474.38 "	WI-17926		ESTs
474.38 "	WI-12790		ESTs, Weakly similar to MULTIDRUG RESI..
474.38 "	1834		EST
474.38 P2.26	sts-X98258	MPP-9	M phase phosphoprotein 9
474.38 P2.39	stSG40753		ESTs
474.64 P>3.00	A004D47		ESTs, Highly similar to There are three pu..
474.64 P>3.00	sts-N23129	MPP-9	M phase phosphoprotein 9
474.75 P2.41	sts-AA040696		ESTs
474.81 P2.37	sts-AA022496		ESTs
474.81 P2.28	stSG46930	MPP-9	M phase phosphoprotein 9
474.97 P>3.00	WI-20552	DRP	density-regulated protein
475.02 P>3.00	SGC30324		ESTs
475.07 P>3.00	D10923	HM74	putative chemokine receptor; GTP-binding pr..
475.07 P>3.00	stSG2418	DOC1	Deleted in oral cancer-1
475.07 "	stSG21321		ESTs
475.07 "	stSG53515	MPP-9	M phase phosphoprotein 9
475.07 P>3.00	SGC31687	DOC1	Deleted in oral cancer-1
475.07 P>3.00	WIAF-214	HM74	putative chemokine receptor; GTP-binding pr..
475.13 P0.79	sts-W93806		ESTs
475.13 P2.13	stSG48145		ESTs
475.18 P2.34	A003B12		Homo sapiens full length insert cDNA clone..

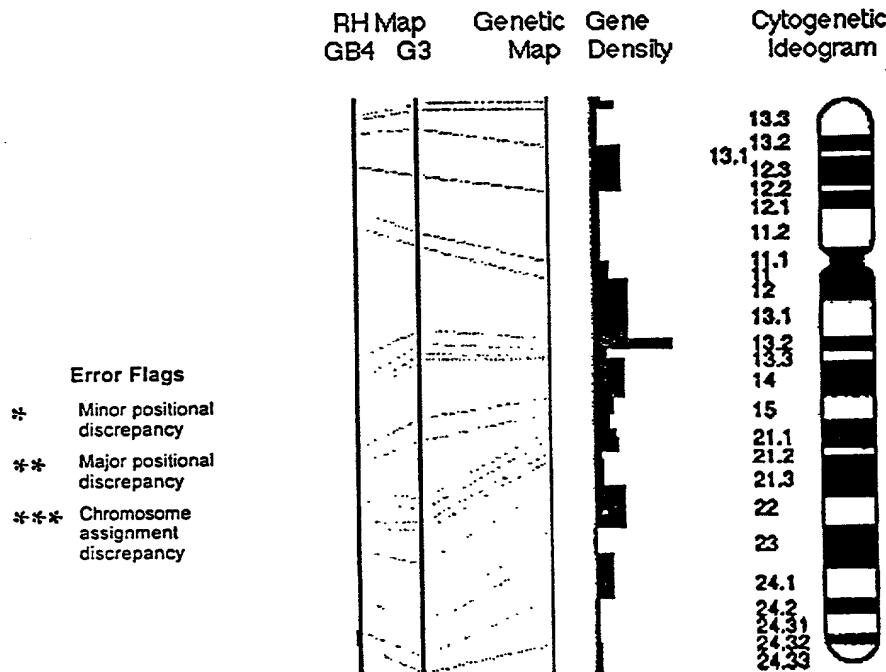
FIG. 2 H

	475.18 P>3.00	WI-22211	Homo sapiens full length insert cDNA clone..
	475.18 P2.08	stSG48093	ESTs
	475.18 "	A004P27	ESTs, Weakly similar to MULTIDRUG RESI..
	475.35 P2.10	stSG9904	ESTs
	475.40 P0.45	sts-AA024696	ESTs
	475.51 P>3.00	stSG53793	ESTs
	476.10 P>3.00	Bda98d05	Homo sapiens full length insert cDNA clone..
	476.21 P>3.00	sts-H24468	ESTs
	476.21 P>3.00	sts-N94741	ESTs
	476.64 P0.28	stSG22488	ESTs
	476.85 P0.36	stSG44909	ESTs
	477.06 P0.10	stSG54797	ESTs
	477.27 P1.33	stSG48099	ESTs
	477.37 P0.09 *	sts-AA028894	Homo sapiens silencing mediator of retinoic..
	477.80 P1.44	stSG52727	EST
	477.80 "	U44799	Human U1-snRNP binding protein homolog mR..
	477.80 "	WI-15963	ESTs
	477.80 "	stSG53886	ESTs, Weakly similar to neuronal thread pr..
	478.74 P0.01	WIAF-364	ESTs
	479.01 P0.21	WI-21080	ESTs
	479.13 P0.19	A009B29	ESTs
	479.33 P0.22	A006F32	EIF2B1 eukaryotic translation initiation factor 2B..
	479.33 P0.19	WIAF-449	EIF2B1 eukaryotic translation initiation factor 2B..
	479.33 P0.19 *	WI-15890	H.sapiens mRNA for transmembrane protein r..
	479.55 P0.20 *	stSG349	H.sapiens mRNA for transmembrane protein r..
	479.55 "	A004O46	BDKRB2 bradykinin receptor B2
	479.55 "	stSG42540	ESTs
	479.55 "	sts-N26791	ESTs
	479.55 "	stSG53943	ESTs
	479.55 "	stSG49468	EST
145.7	479.74 P0.16	AFM294ze9	D12S342 Microsatellite marker AFM294ze9
	481.46 P0.00	sts-AA007694	EST
147.5	481.56 F	AFM294xg1	D12S340 Microsatellite anchor marker AFM294xg1

↓ Next interval down

FIG. 21

Chromosome 12: D12S340-D12S97



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

Physical size of bin: 13 cR3000

147.5	←	◆	481.56 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1
			481.66 P0.00	SGC31838		ESTs
			483.18 P0.70	stSG48255		ESTs
			483.58 P0.69	stSG47315		ESTs

FIG. 2 J

483.87 P0.83	stSG47707		ESTs
484.70 P0.93	stSG4060		ESTs
484.70 "	stSG62390	GTF2H3	general transcription factor IIH, polypepti..
484.70 "	stSG42994		ESTs
484.73 P0.74	stSG46906		ESTs
484.80 P0.91	A004X33		ESTs
484.91 P1.11	stSG3211		ESTs, Weakly similar to B-cell growth fact..
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 " *	sts-Z41302	BDKRB2	bradykinin receptor B2
484.91 "	sts-T58259		ESTs, Weakly similar to B-cell growth fact..
484.91 "	stSG52737		ESTs
484.91 "	Bda03b10	UBC	ubiquitin C
484.91 "	stSG1936	CD36L1	CD36 antigen (collagen type I receptor, thr..
484.91 "	sts-AA017225		ESTs
484.91 P1.15	WI-12212		ESTs
485.12 P1.18	A004F14		ESTs
485.12 P1.18	SGC31333		ESTs
485.23 P1.21 *	WI-12482	BDKRB2	bradykinin receptor B2
485.23 P1.07	sts-AA017698		ESTs
485.33 P1.22	WI-12422		ESTs
485.51 P1.18	stSG42398		EST
485.64 P1.04	sts-AA009669		ESTs
486.07 P2.50	stSG21539		EST
486.13 P1.44	WI-12439		EST
486.34 P1.26	sts-W31616	UBC	ubiquitin C
486.38 P>3.00	stSG54715		ESTs
486.76 P1.64 *	WI-6921		H.sapiens mRNA for transmembrane protein r..
487.08 P>3.00	WI-13120		Human mRNA for KIAA0318 gene, partial cds
487.23 P>3.00	stSG54353		ESTs
487.23 P>3.00	stSG22703		EST
487.28 P>3.00	stSG62698		ESTs
487.28 P>3.00 *	sts-D60472		Homo sapiens silencing mediator of retinoic..
487.28 P>3.00	stSG36097		ESTs
487.33 P1.36	sts-U37146		Homo sapiens silencing mediator of retinoic..

FIG. 2 K

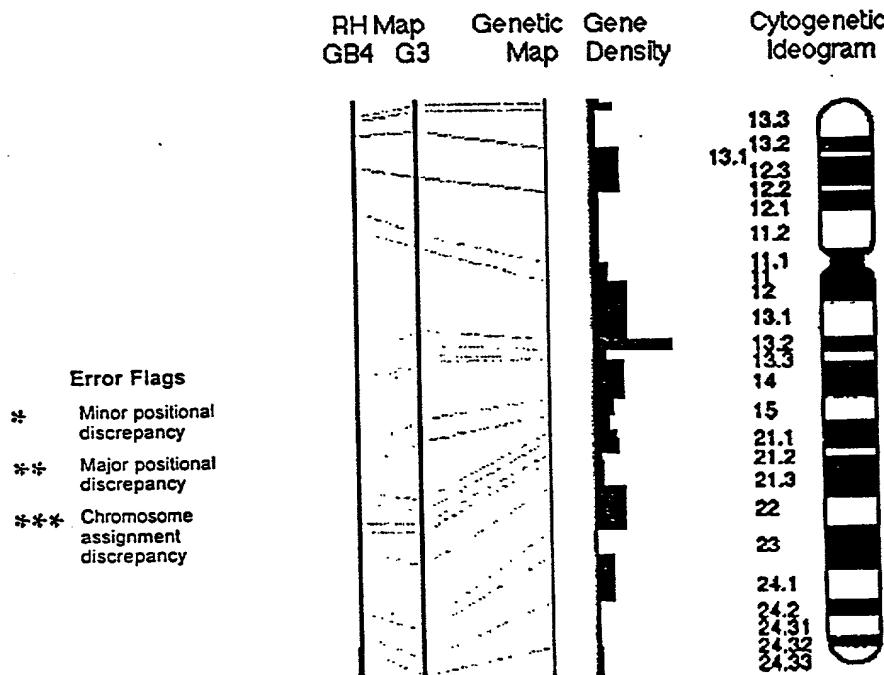
	487.50 P>3.00	stSG9807	ESTs
	487.50 P>3.00	stSG15434	ESTs
	487.60 P>3.00	stSG53251	ESTs
	487.60 P>3.00	stSG30525	SRRP129 SC35-interacting protein 1
	487.60 P>3.00	stSG46424	ESTs
	487.70 P>3.00	A007A34	ESTs
154.4	487.75 P2.00	AFMa197zd9	D12S1609 Microsatellite marker AFMa197zd9
	487.75 P2.02	A006D44	ESTs
	487.80 P>3.00	SGC30248	ESTs, Weakly similar to peptide/histidine ..
	488.07 P1.68	stSG6320	Homo sapiens clone 24617 mRNA sequence
	488.07 P1.66	stSG6305	Homo sapiens clone 24790 mRNA sequence
	488.07 P0.02	sts-N20163	Homo sapiens full length insert cDNA clone..
	488.12 P>3.00	stSG60065	ESTs
	488.12 P>3.00	stSG47723	ESTs
	488.44 P1.59	stSG3292	Homo sapiens clone 24790 mRNA sequence
	488.44 P0.03	WIAF-856	EST, Weakly similar to reverse transcripta..
	488.65 P1.54	WI-12272	Homo sapiens clone 24790 mRNA sequence
	488.65 P1.82	stSG52343	ESTs
	488.82 P1.80	stSG16387	CPN2 carboxypeptidase N, polypeptide 2, 83kD
	488.97 P1.80	SGC31722	ESTs
	489.07 P0.06	stSG54325	ESTs
	489.07 P>3.00	stSG63473	ESTs
160.9	♦ 489.07 P>3.00	AFMa123xe1	D12S367 Microsatellite marker AFMa123xe1
	489.14 P0.17	sts-T81113	ESTs
	489.29 P0.05	sts-AA025438	EST
	489.50 P1.37	***	Cdalad08 ESTs
	489.50 P0.05	WI-15018	ESTs
	489.50 P1.50	WI-18492	ESTs
	489.57 P1.48	WI-16177	Homo sapiens androgen receptor associated p..
	489.67 P1.44	stSG53307	ESTs
	489.71 P1.43	stSG53541	Homo sapiens hiwi mRNA, partial cds
	489.71 P1.43	stSG9546	Homo sapiens clone 24617 mRNA sequence
	489.89 P1.56	A006O16	ESTs
	490.10 P1.42	H64839	EST

FIG. 2 L

160.9 | 490.20 P0.05 stSG43910 SFRS8 splicing factor, arginine/serine-rich 8 (sup..
 ♦ 494.19 F AFM210zd6 D12S97 Microsatellite anchor marker AFM210zd6
Next interval down

FIG. 2 M

Chromosome 12: D12S97-qTEL



The interval shown is on the GB4 map

See also: equivalent interval on G3 map

About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: 172 cR3000

160.9	494.19 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6
	498.06 P0.02	stSG53600		ESTs, Weakly similar to peptide/histidine ..
	499.71 P1.73	stSG3357		ESTs
165.7	499.71 "	AFM295ye9	D12S343	Microsatellite marker AFM295ye9

FIG. 2 N

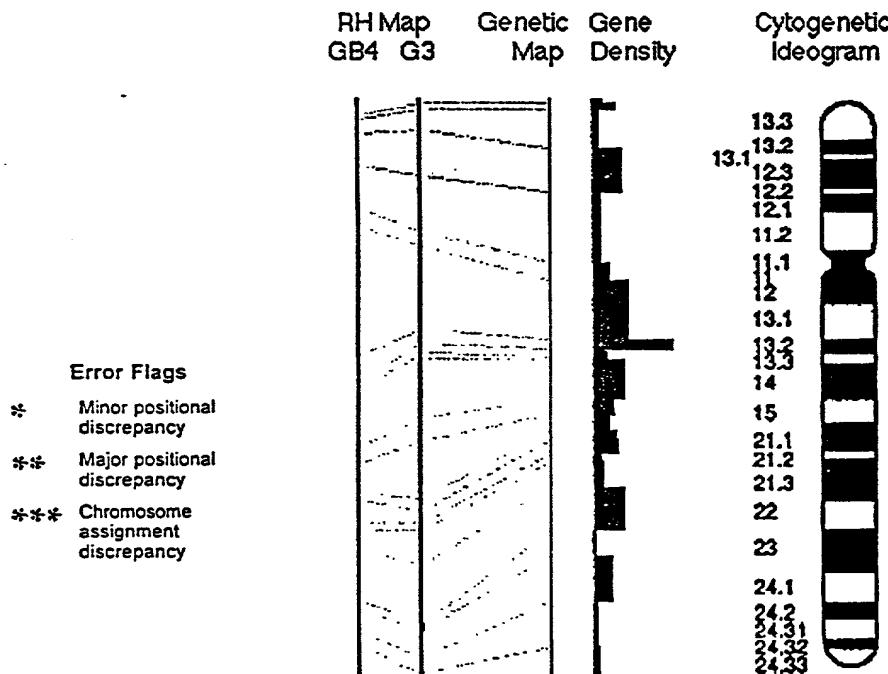
499.71 P1.72	stSG30906		ESTs
499.71 "	stSG43796	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.71 P1.71	sts-X89576	MMP17	matrix metalloproteinase 17 (membrane-insert..
499.92 P>3.00	stSG43769		ESTs
500.50 P1.88	stSG26056		ESTs
500.50 P2.33	SGC30786	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG1702		Homo sapiens CAGH32 mRNA, partial cds
500.61 "	sts-N59820		ESTs
500.61 "	stSG42115	KIAA0331	KIAA0331 gene product
500.61 "	IB2452	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 "	stSG52521		ESTs
500.61 "	FB9F8		ESTs, Weakly similar to PUTATIVE ATP-D..
500.61 "	AA252357		ESTs
500.61 "	stSG4720		Homo sapiens pseudouridine synthase 1 (PUS..
500.61 "	sts-AA001424	KIAA0331	KIAA0331 gene product
500.61 P>3.00	stSG31443		ESTs
500.61 P>3.00	stSG49622	ULK1	unc-51 (C. elegans)-like kinase 1
500.61 P2.49	stSG50559		ESTs
501.04 P1.10	stSG54842		ESTs
501.04 P2.03	A008Y05		Unknown
501.89 P2.18	stSG39493		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	A002A44		Homo sapiens CAGH32 mRNA, partial cds
501.99 P>3.00	sts-H94865		EST
501.99 P>3.00	R50113		ESTs
502.10 P1.75	stSG48386		ESTs
502.10 "	stSG50504		ESTs
502.63 P0.06	A006R19		ESTs
502.63 P1.06	WIAF-864		ESTs
502.94 P1.51	stSG54813		ESTs, Weakly similar to peroxisome membran..
503.04 P1.42	A004B47		ESTs, Highly similar to DNA polymerase εp..
503.25 P0.28	stSG27206		ESTs
503.25 "	stSG40199		Homo sapiens mRNA for KIAA0692 protein, p..
503.46 P0.23	stSG8935		ESTs
504.68 P0.69	stSG4731		Homo sapiens mRNA for KIAA0692 protein, p..

FIG. 2 O

	504.68 "	A005Q05	ESTs
	504.68 "	stSG8142	ESTs, Highly similar to DNA polymerase ep..
169.1	506.39 F	AFM310vd5 D12S357	Microsatellite marker AFM310vd5
	506.39 P0.02	A005X42	Homo sapiens mRNA for KIAA0692 protein, p..
	508.59 P0.78	Cda18g06	ESTs
◆	508.59 P0.78 **	Cda1jf08	Homo sapiens mRNA for GCP170, complete cd..
	508.59 P0.54	R39599	ESTs
	509.98 P0.10	stSG31494 ZNF140	zinc finger protein 140 (clone pHZ-39)
	509.98 P0.16	stSG40222	ESTs
	509.98 "	sts-R55615	ESTs, Weakly similar to zinc finger protei..
	509.98 "	sts-R02295	ESTs
	509.98 "	sts-R81342	ESTs
	511.20 F	TEL-12q82	Marker TEL-12q82
	512.81 P0.20	sts-H65839	ESTs, Weakly similar to transformation-rel..
	514.97 P0.36	stSG46141	ESTs, Weakly similar to zinc finger protei..
	514.97 P0.90	stSG52998	ESTs
	519.10 P1.77	A008W21 CYP51	cytochrome P450, 51 (lanosterol 14-alpha-de..
	519.54 P0.81	stSG52716	ESTs

TELOMERE

Chromosome 12: D12S79-D12S366



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S79 (126.1 cM)

Bottom of interval: D12S366 (133.8 cM)

Genetic size of bin: 8 cM

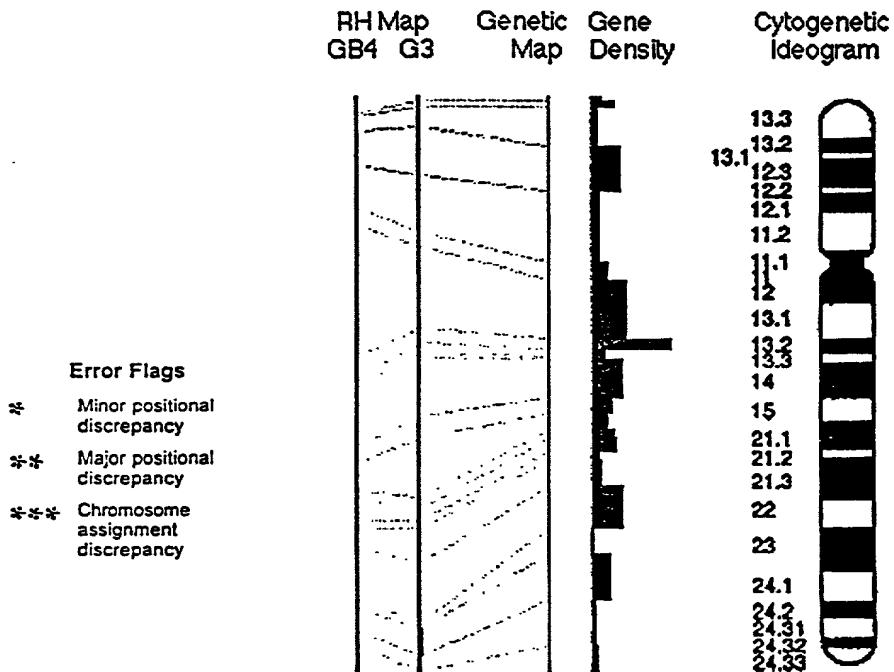
Physical size of bin: 63 cR10000

FIG. 3 A

		Next interval up
126.1	◆ 4955 F	AFM067yc5 D12S79 Microsatellite anchor marker AFM067yc5 (SHGC-692)
129.2	4988 F	AFMa067we1 D12S1718 Microsatellite marker AFMa067we1 (SHGC-20..
	◆ 5007 F *	SHGC-2657 Homo sapiens clone 23714 mRNA sequence
	◆ 5014 F *	SHGC-2653 Homo sapiens clone 23714 mRNA sequence
133.8	◆ 5018 F	AFM351tb9 D12S366 Microsatellite anchor marker AFM351tb9 (SHGC-2155)
		Next interval down

FIG. 3 B

Chromosome 12: D12S366-D12S340



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S366 (133.8 cM)

Bottom of interval: D12S340 (147.5 cM)

Genetic size of bin: 14 cM

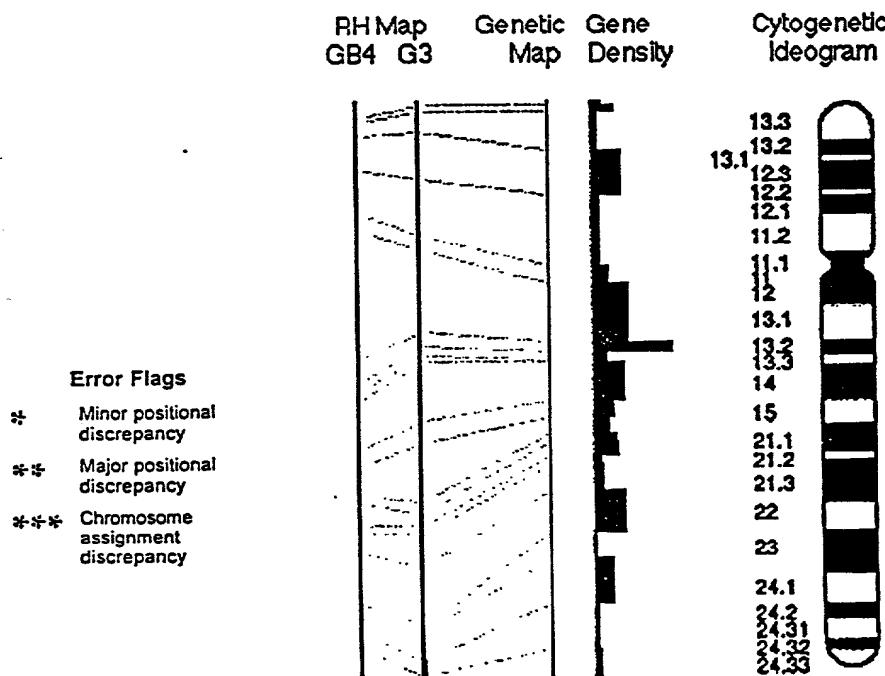
Physical size of bin: 261 cR10000

FIG. 3 C

			Next interval up
133.8	◆ 5018 F	AFM351tb9	D12S366 Microsatellite anchor marker AFM351tb9 (SHGC-2155)
135.1	5047 F	AFMa225xe5	D12S1619 Microsatellite marker AFMa225xe5 (SHGC-20..)
	◆ 5085 F	SHGC-33949	KIAA0262 KIAA0262 gene product
	◆ 5089 F	SHGC-10488	KIAA0152 KIAA0152 gene product
	◆ 5093 F	SHGC-10346	Homo sapiens HSPC004 mRNA, complete cds
	◆ 5098 F	SHGC-13898	Homo sapiens HSPC004 mRNA, complete cds
137.5	◆ 5163 F	AFM220zf4	D12S321 Microsatellite marker AFM220zf4 (SHGC-212..)
	5199 F	SHGC-11702	ESTs
147.5	◆ 5279 F	AFM294xg1	D12S340 Microsatellite anchor marker AFM294xg1 (SHGC-2134)
			Next interval down

FIG. 3 D

Chromosome 12: D12S340-D12S97



About This Interval

Top of interval: D12S340 (147.5 cM)

Bottom of interval: D12S97 (160.9 cM)

Genetic size of bin: 13 cM

Physical size of bin: 151 cR10000

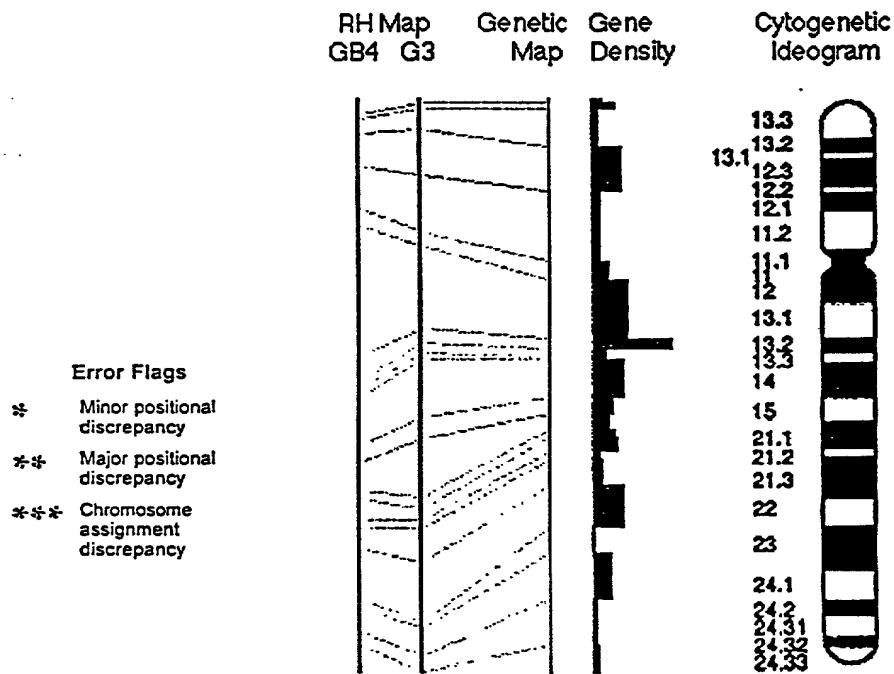
FIG. 3 E

↑ Next interval up

147.5	◆ 5279 F	AFM294xg1	D12S340	Microsatellite anchor marker AFM294xg1 (SHGC-2134)
148.3	5288 F	AFM234tb10	D12S324	Microsatellite marker AFM234tb10 (SHGC-21..)
154.4	5316 F	AFMb350zb5	D12S1679	Microsatellite marker AFMb350zb5 (SHGC-20..)
149.5	5358 F	AFM198wh2	D12S307	Microsatellite marker AFM198wh2 (SHGC-211..)
157.2	5393 F	AFMb301we5	D12S1659	Microsatellite marker AFMb301we5 (SHGC-20..)
160.9	◆ 5415 F	AFMa123xe1	D12S367	Microsatellite marker AFMa123xe1 (SHGC-21..)
160.9	◆ 5430 F	AFM210zd6	D12S97	Microsatellite anchor marker AFM210zd6 (SHGC-372)

FIG. 3 F

Chromosome 12: D12S97-qTEL



The interval shown is on the G3 map

See also: equivalent interval on GB4 map

About This Interval

Top of interval: D12S97 (160.9 cM)

Bottom of interval: chr12_qTEL (169.1 cM)

Genetic size of bin: 8 cM

Physical size of bin: -4429 cR10000

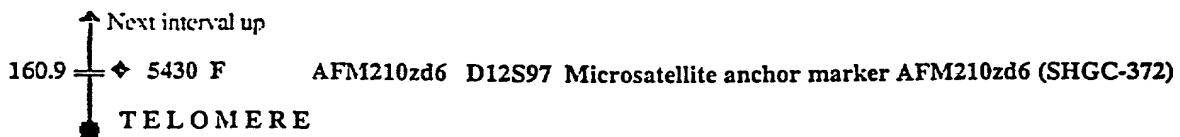


FIG. 3 G

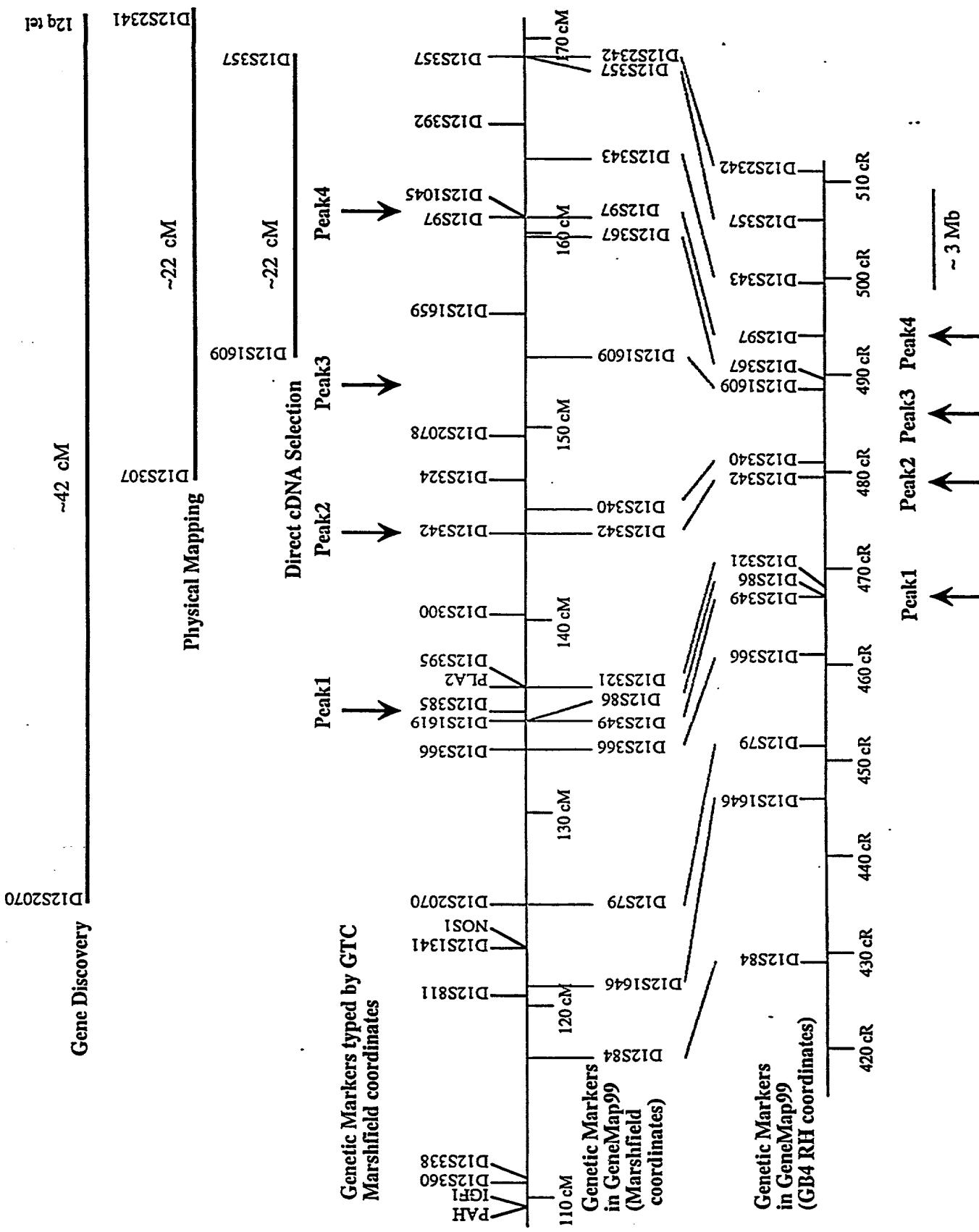


FIG. 4

FIG. 5A

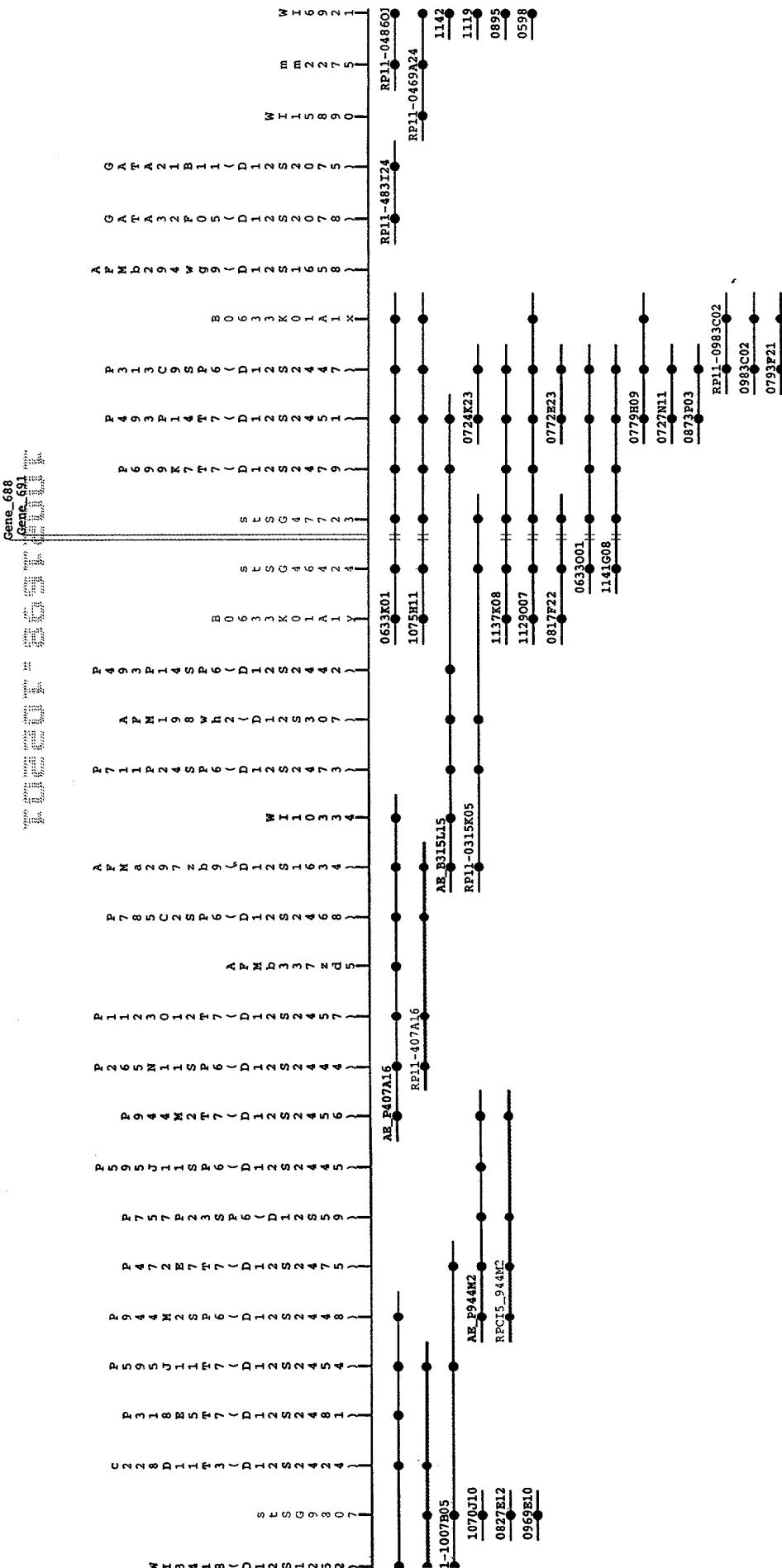
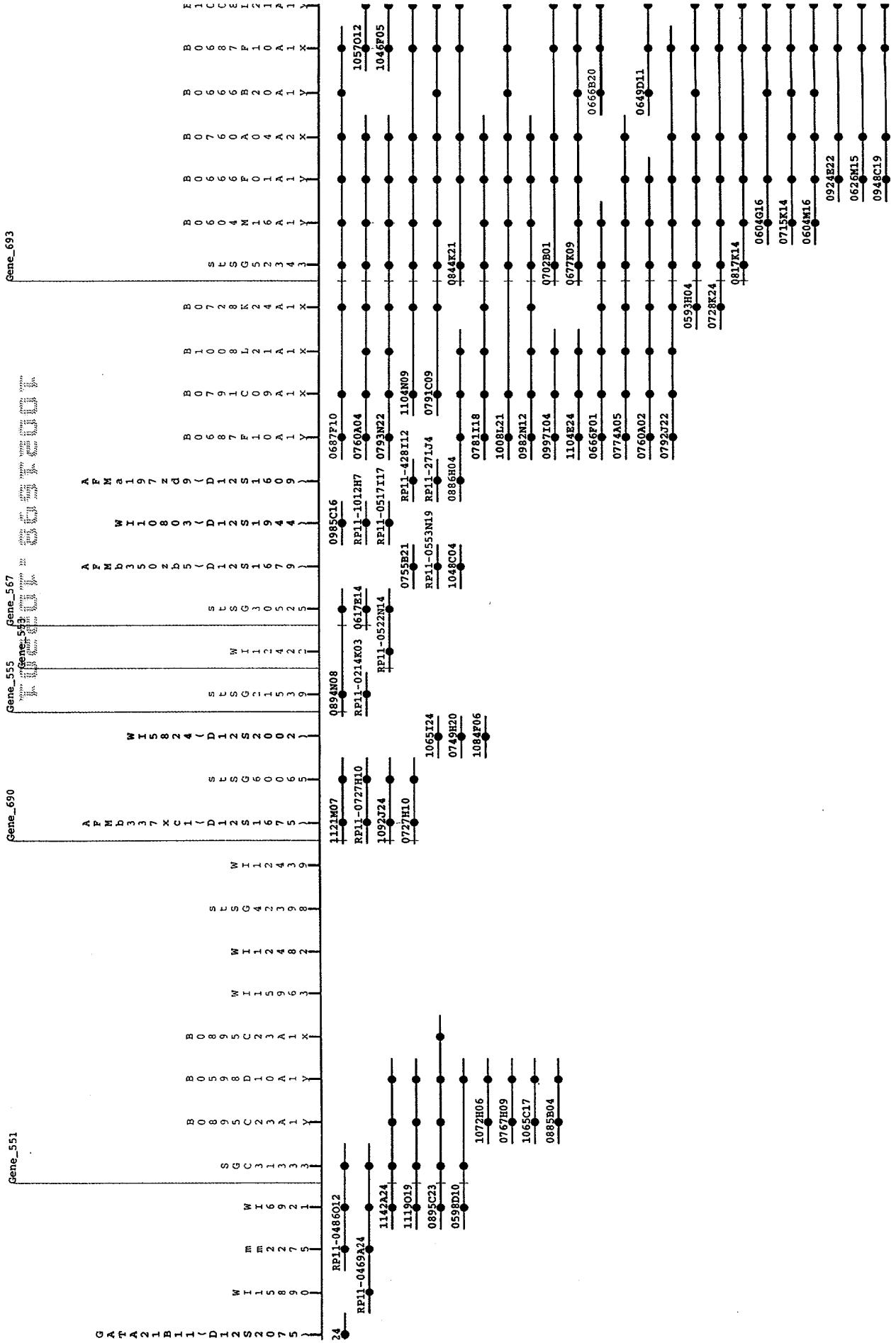


FIG. 5B



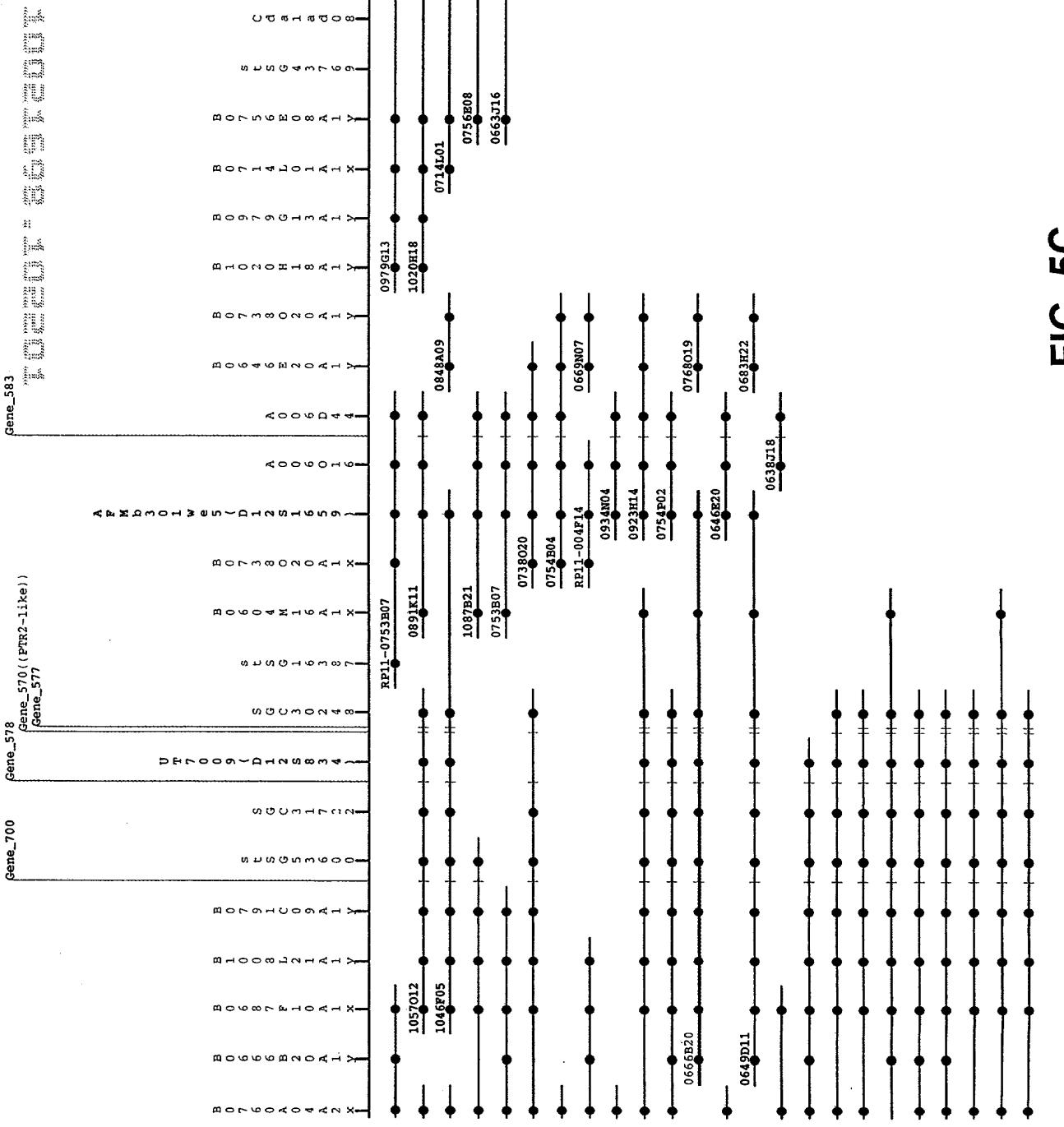


FIG. 5C

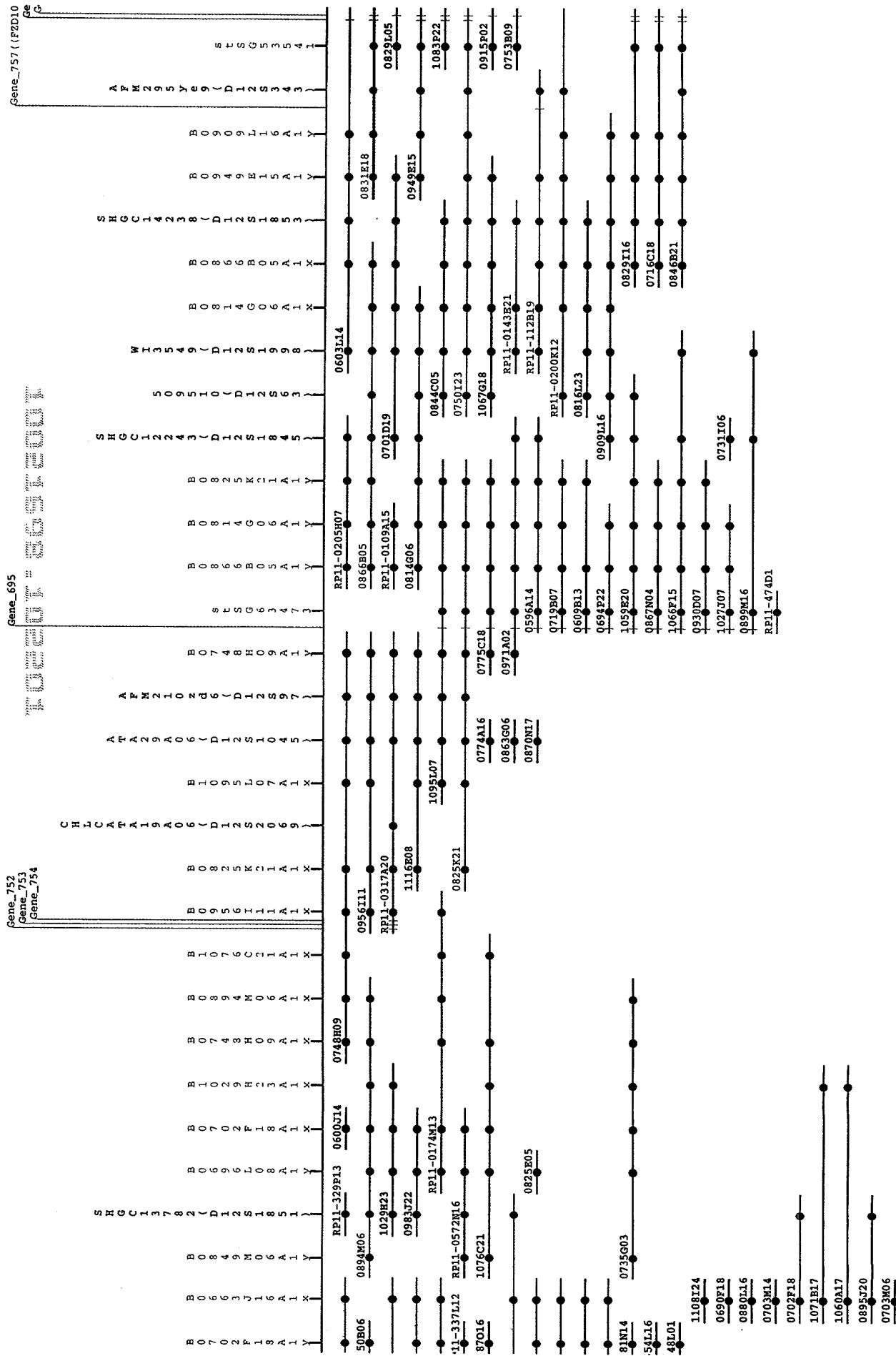


FIG. 5D

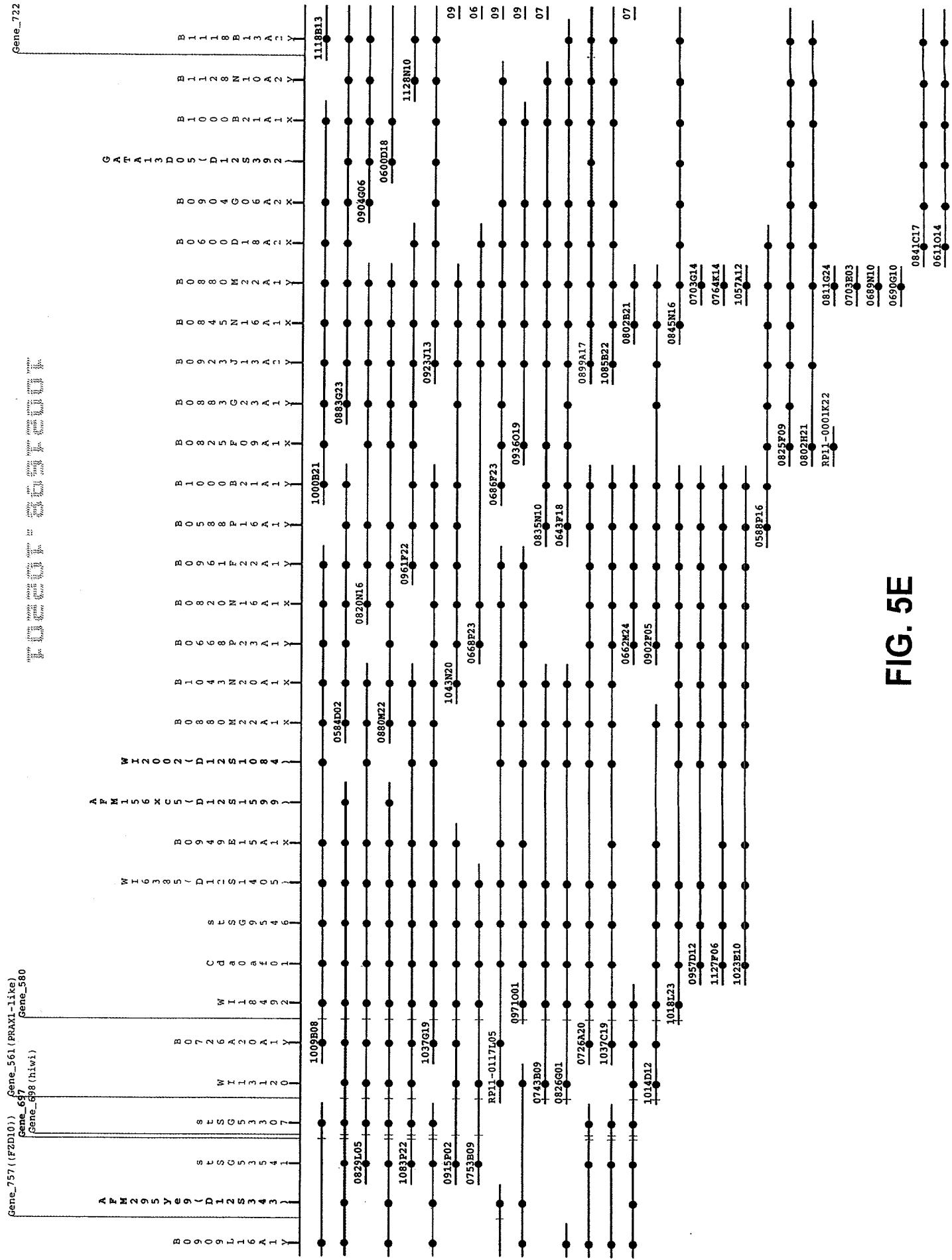


FIG. 5E

FIG. 5F

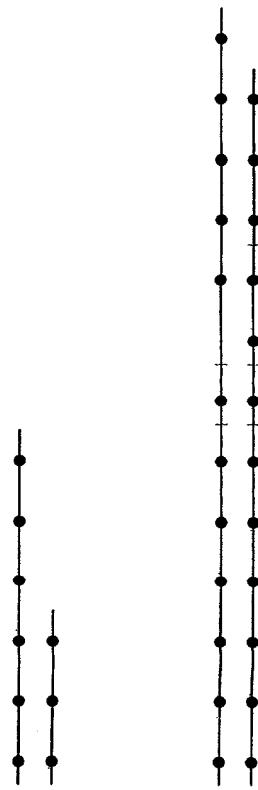
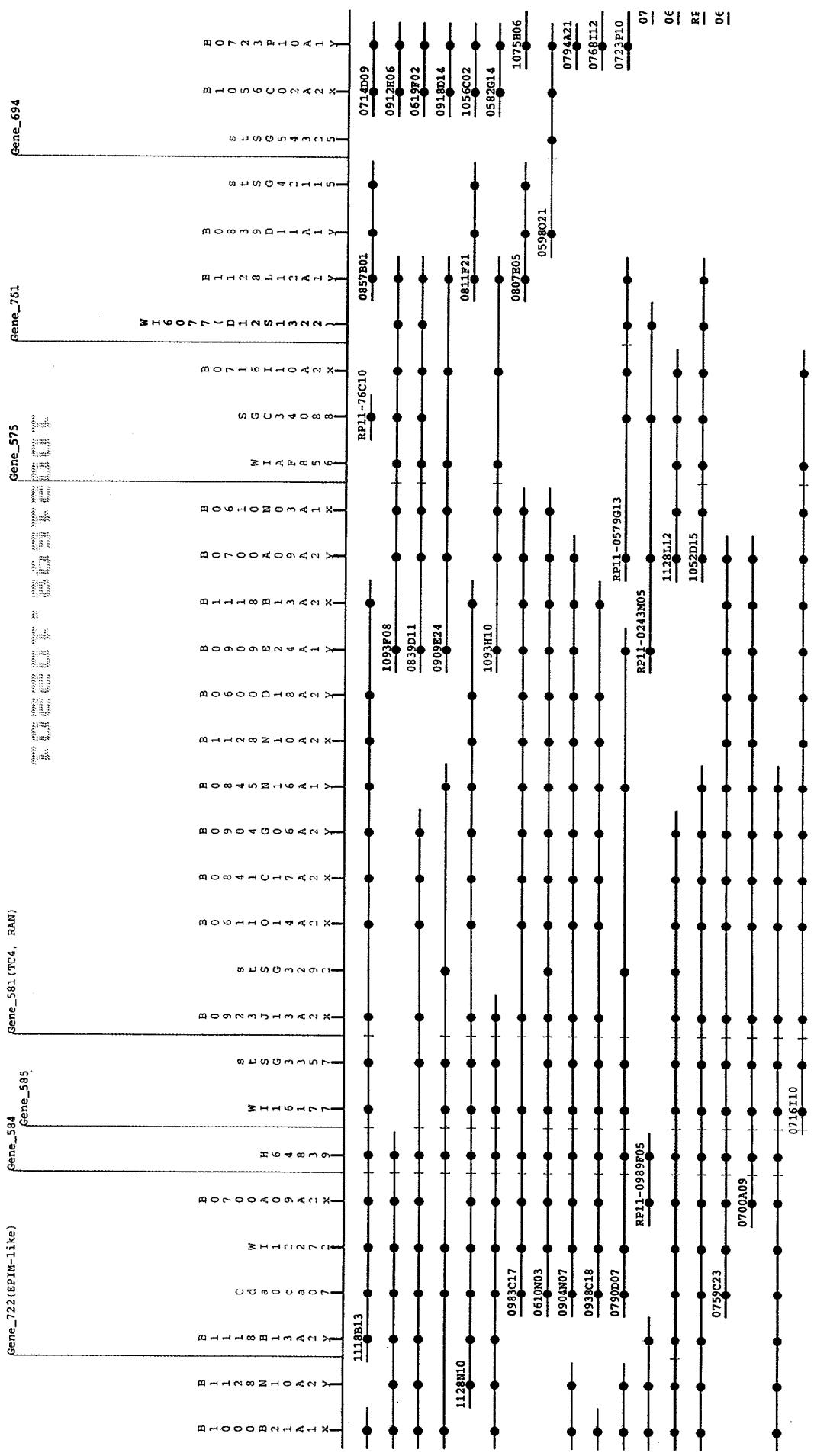


FIG. 5G

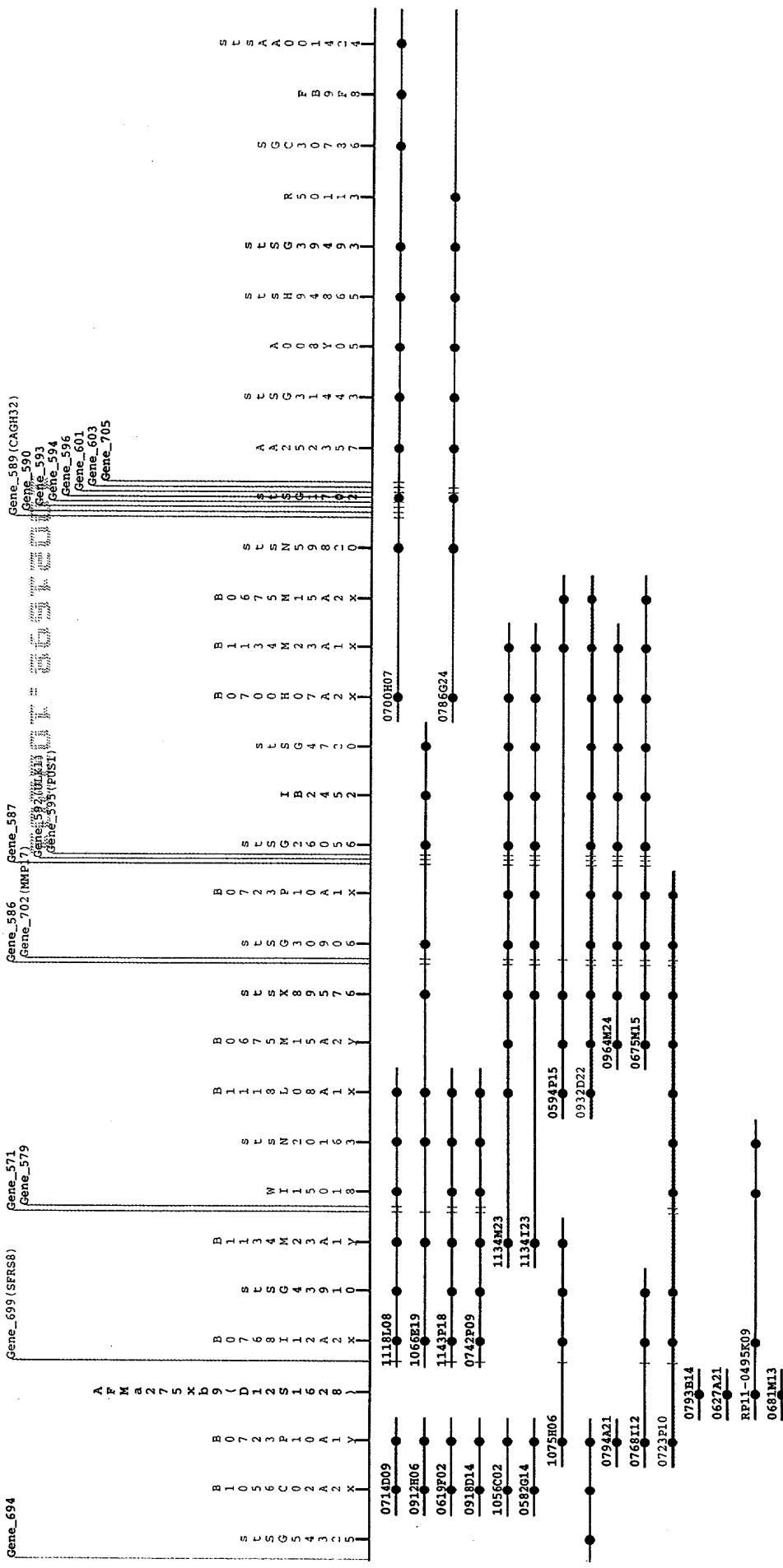


FIG. 5H

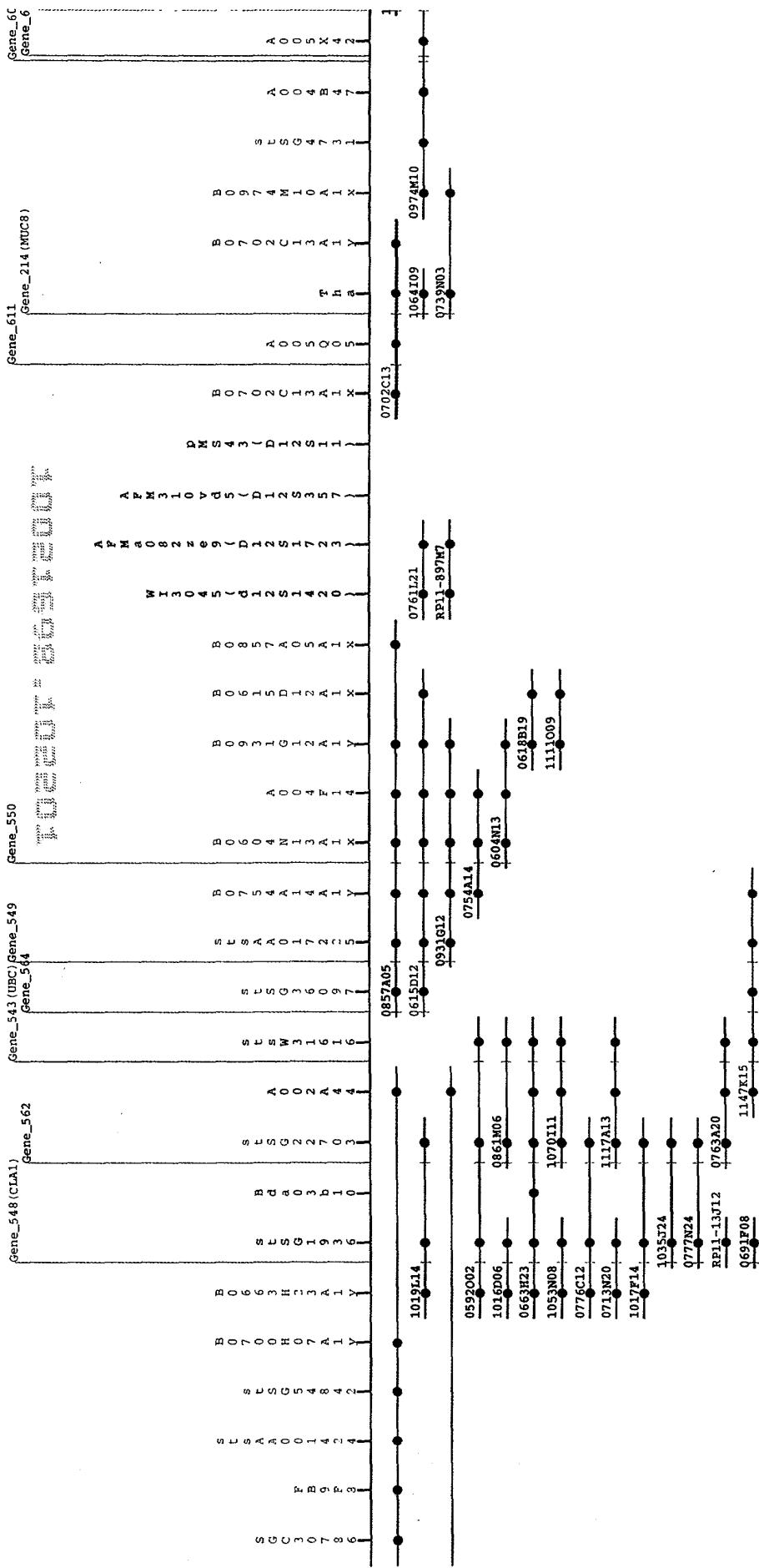
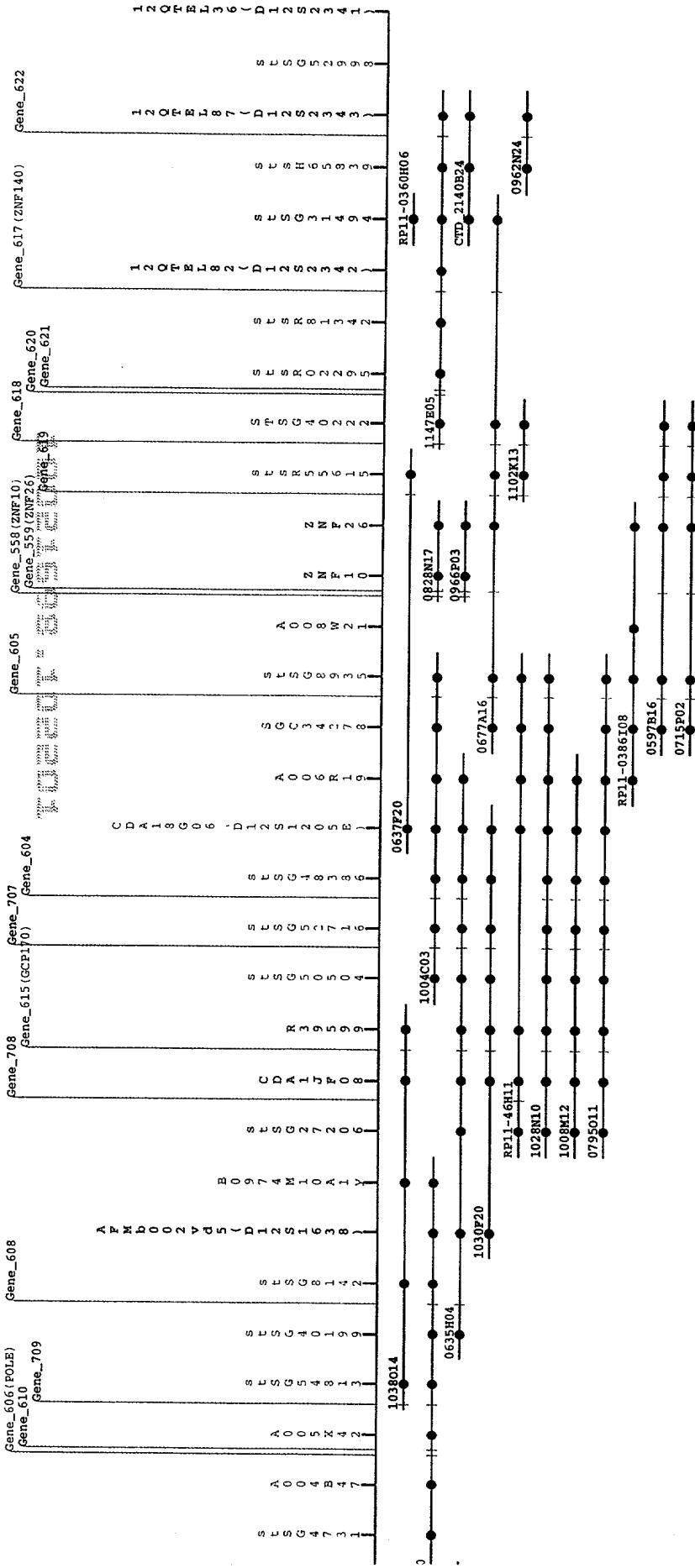
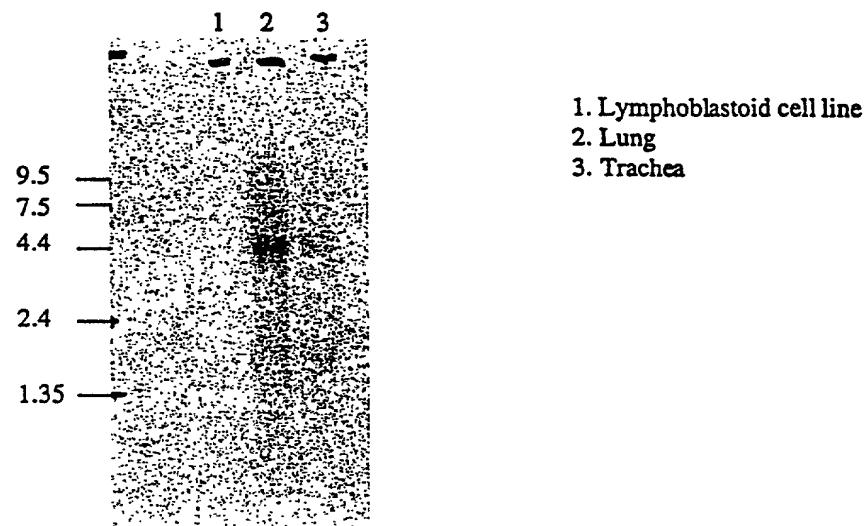


FIG. 5I

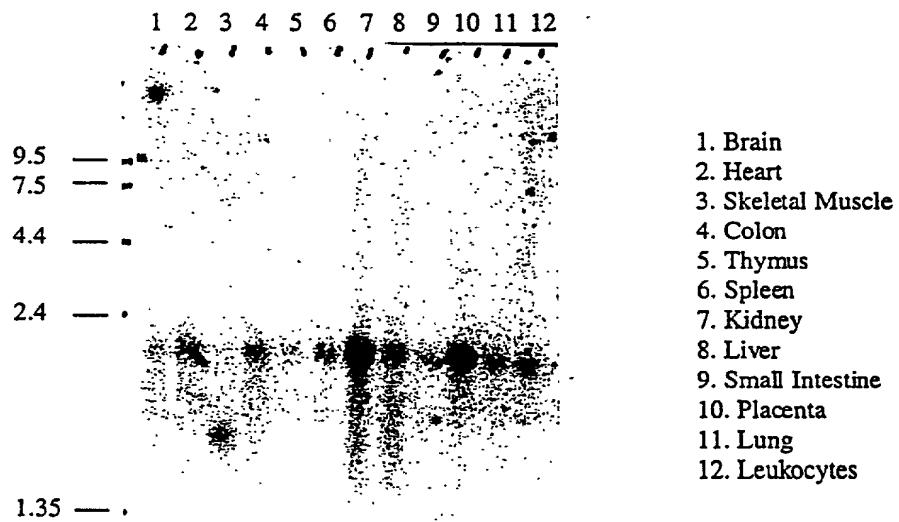


Gene 214



1. Lymphoblastoid cell line
2. Lung
3. Trachea

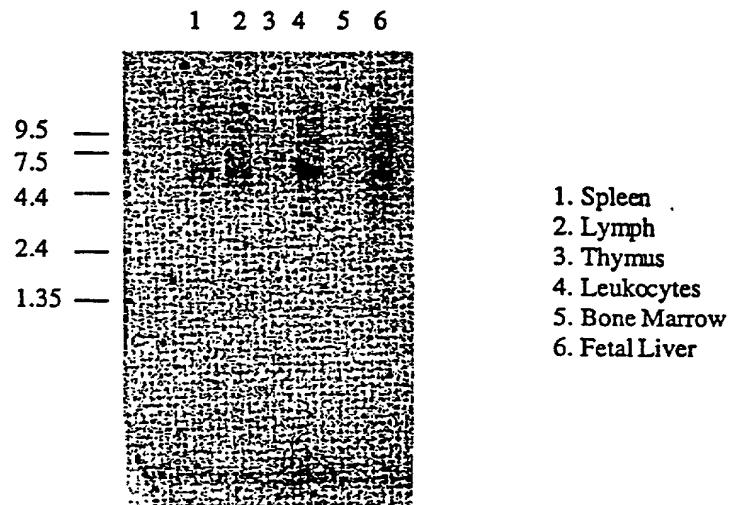
Gene 436



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 A

Gene 454



Gene 515

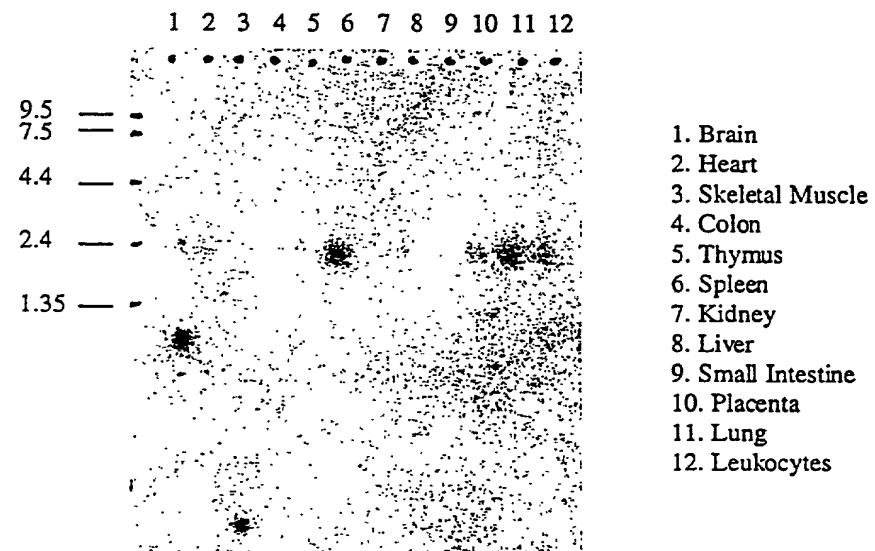
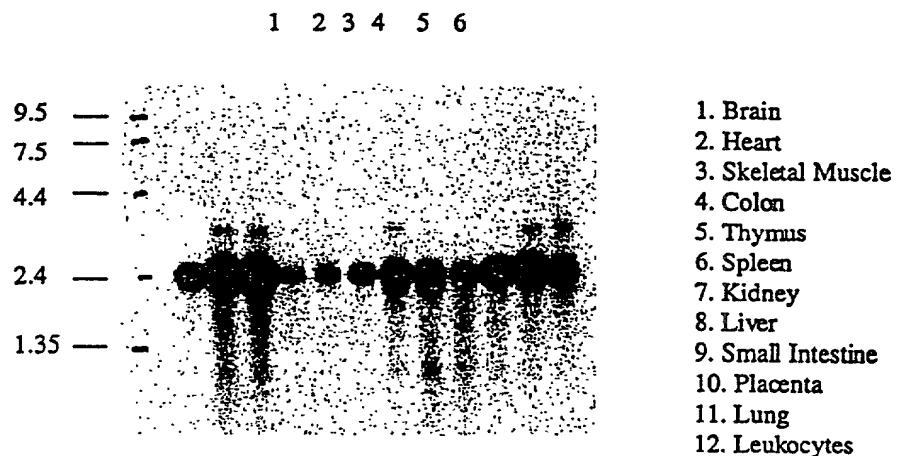


FIG. 6 B

Gene 543



Gene 548

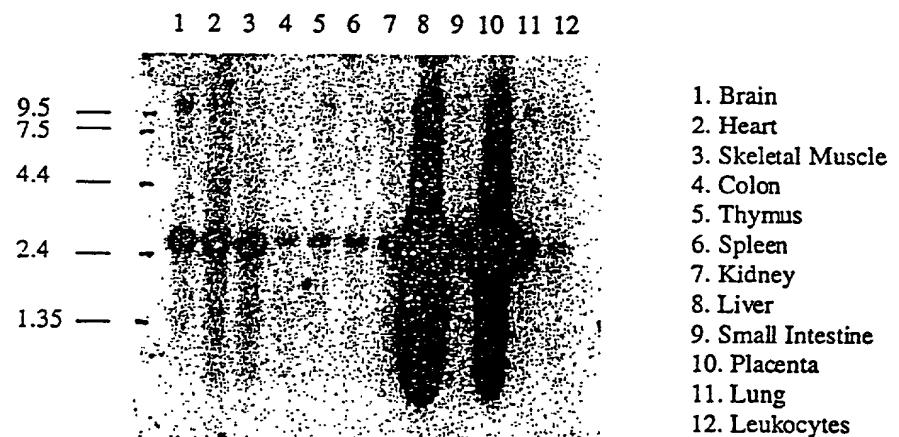
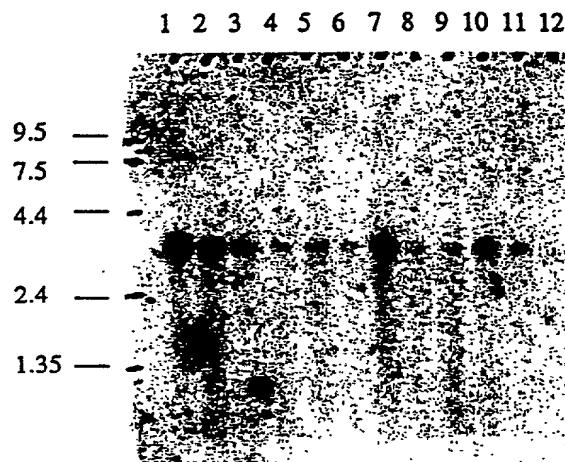


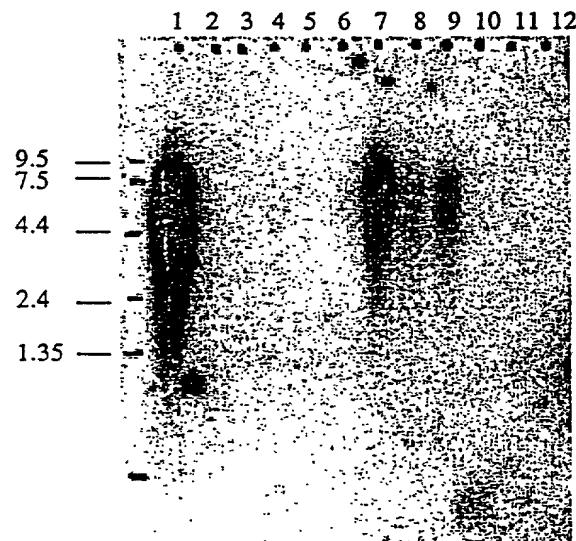
FIG. 6 C

Gene 550



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

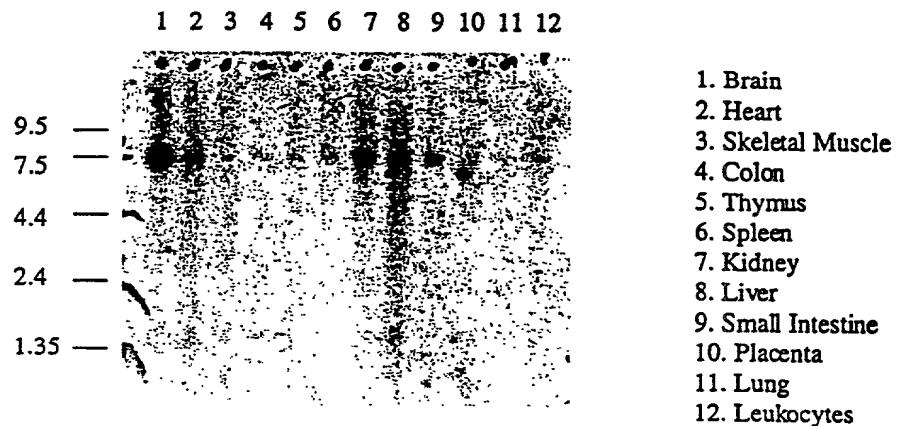
Gene 561



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 D

Gene 564



Gene 570

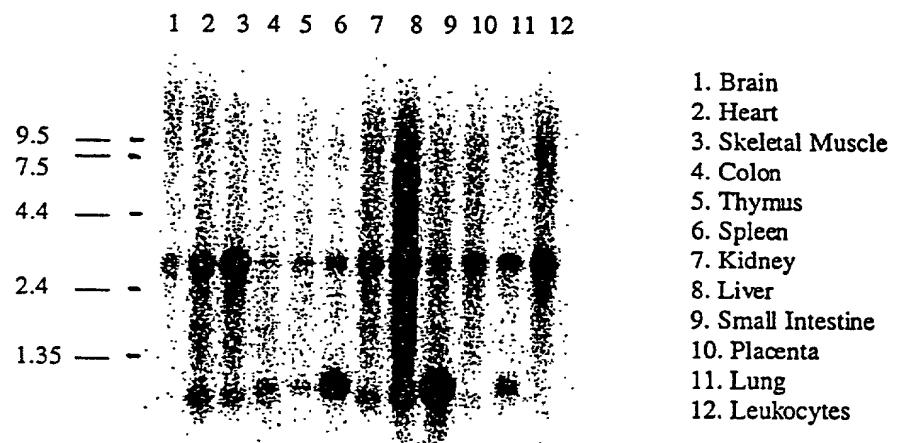
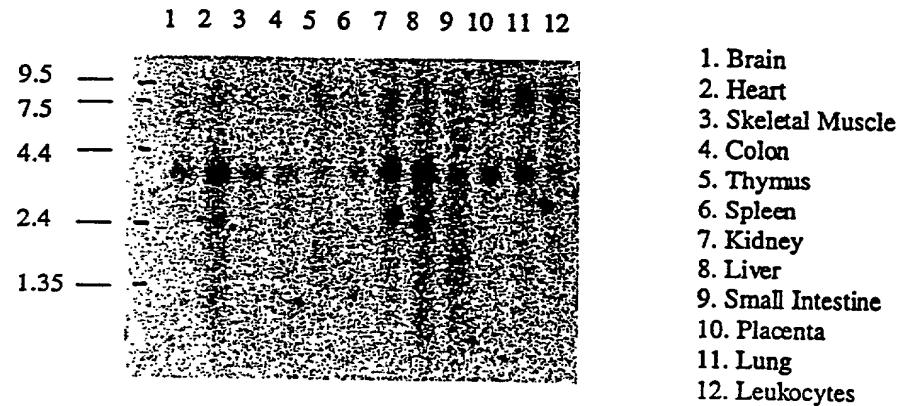


FIG. 6 E

Gene 576



Gene 577

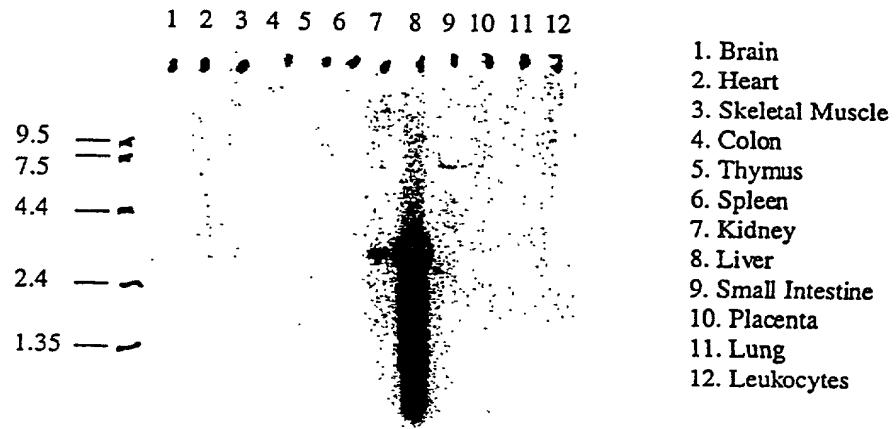
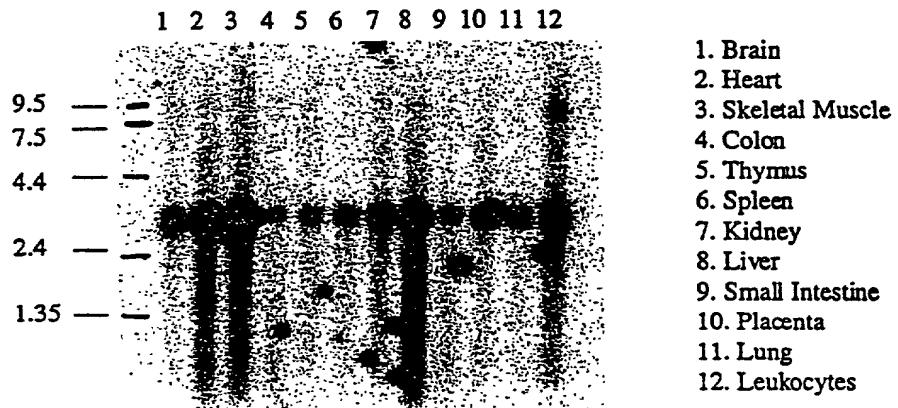


FIG. 6 F

Gene 578



Gene 579

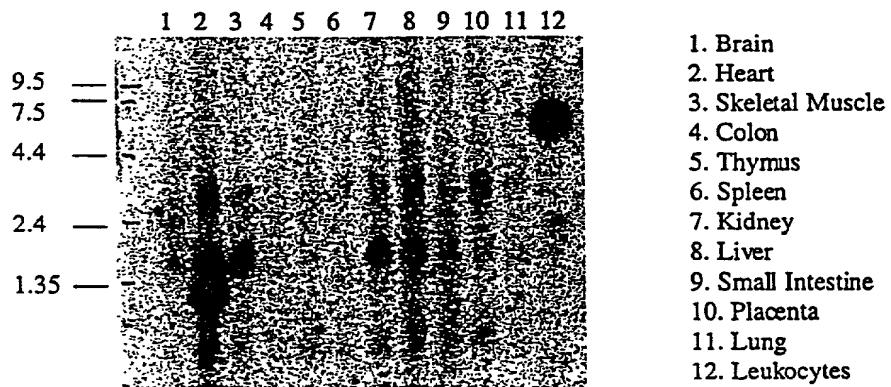
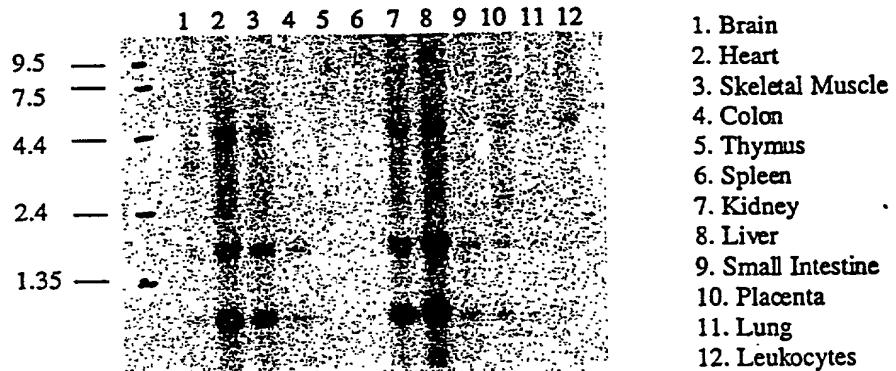


FIG. 6 G

Gene 580



Gene 581

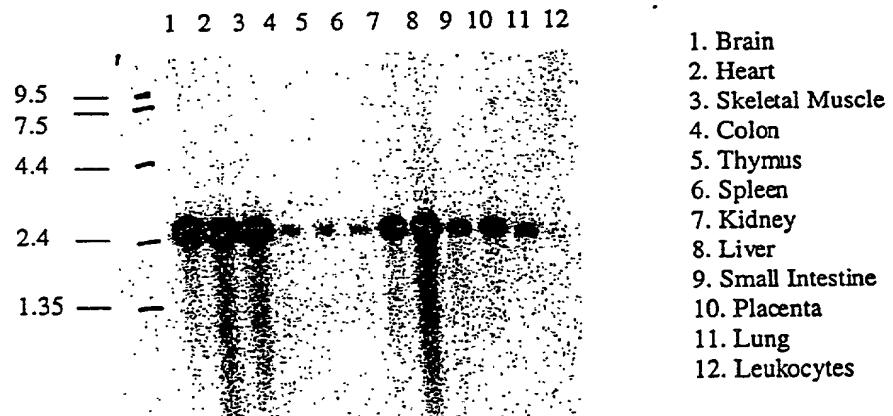
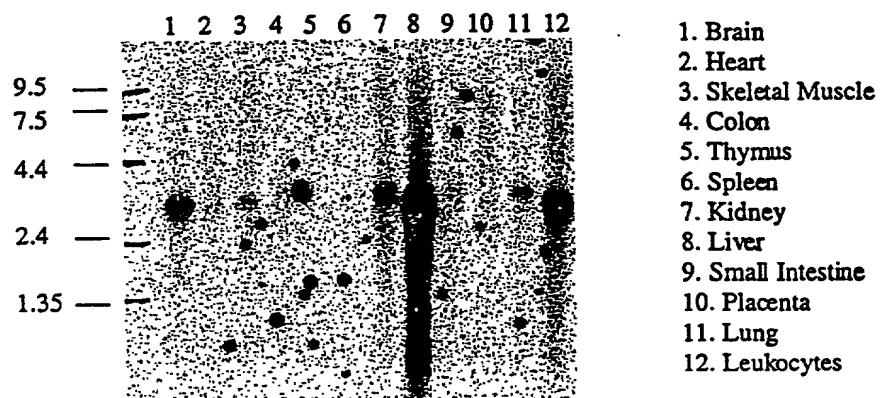


FIG. 6 H

Gene 583



Gene 589

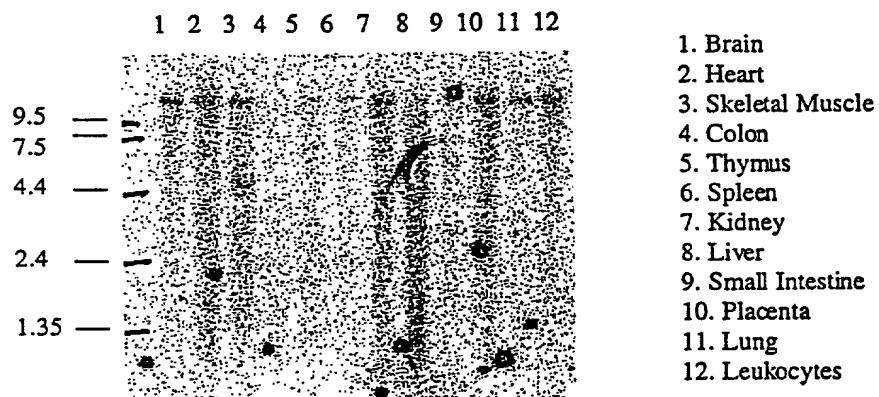
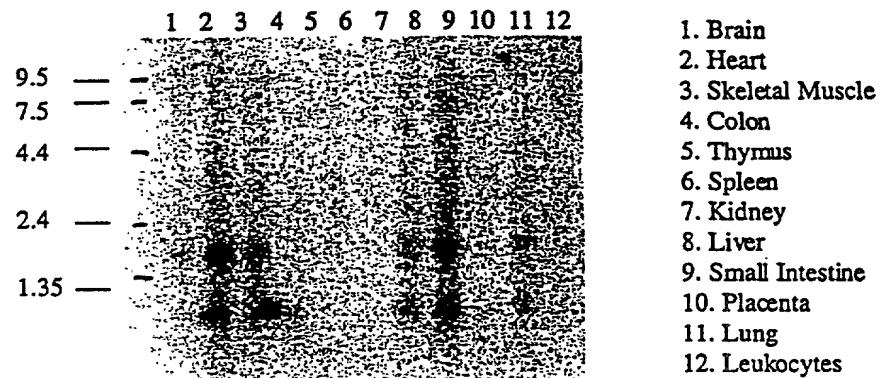


FIG. 6 I

Gene 590



Gene 592

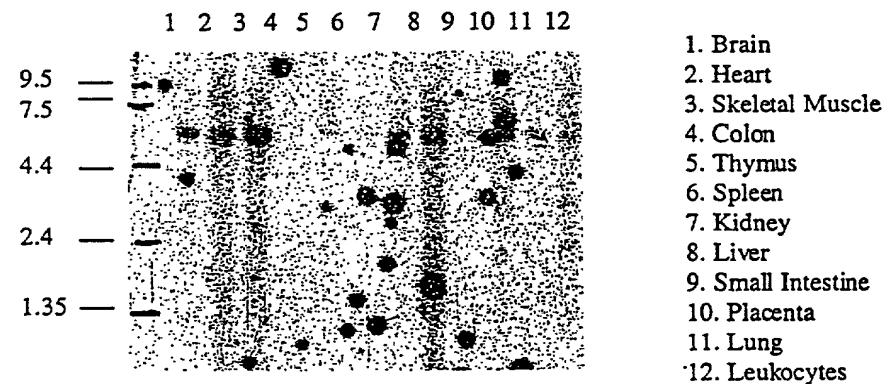
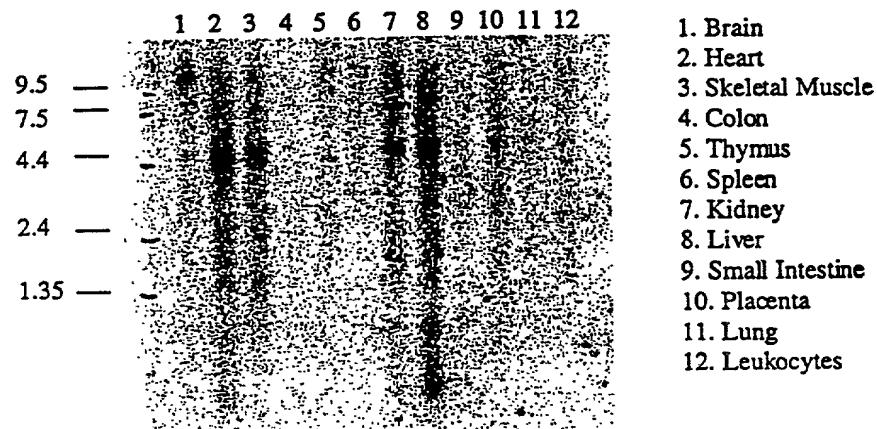


FIG. 6 J

Gene 594



Gene 595

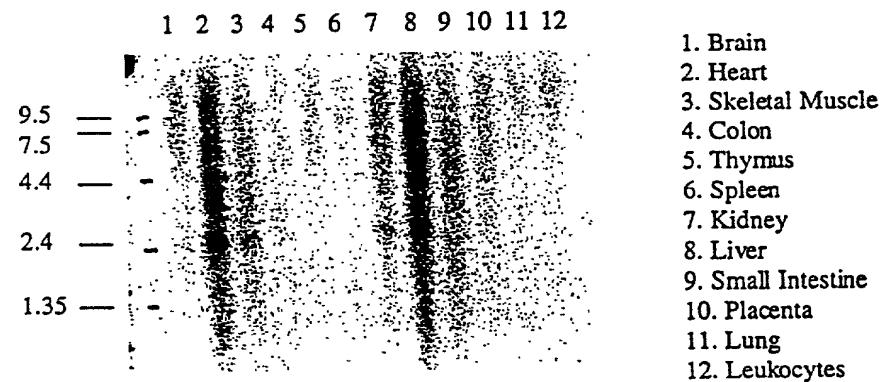
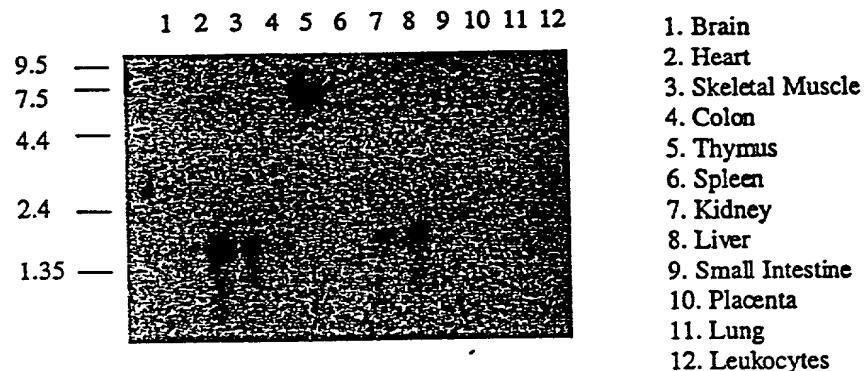


FIG. 6 K

Gene 596



Gene 604

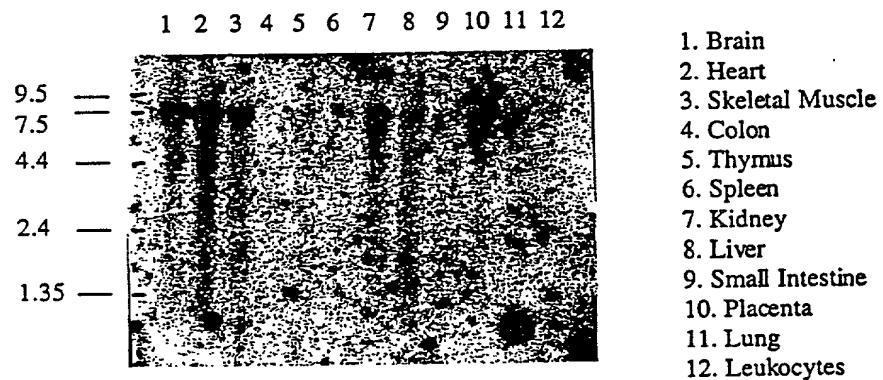
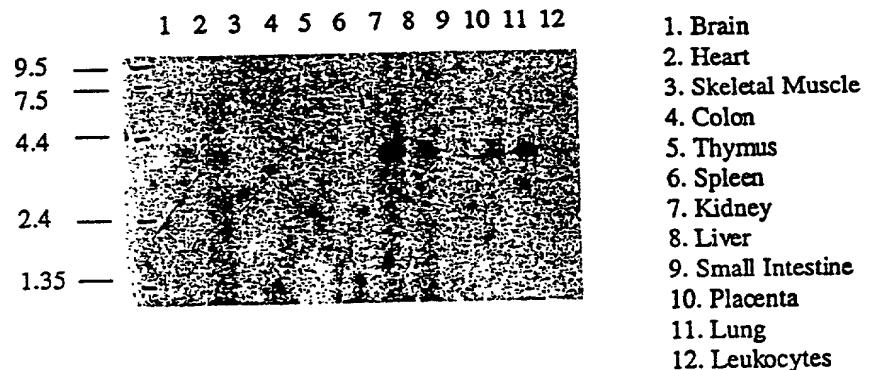


FIG. 6 L

Gene 605



Gene 606

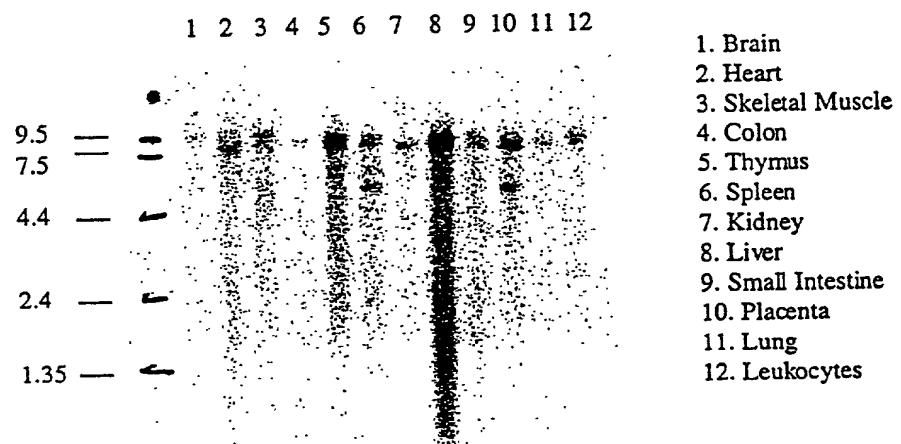
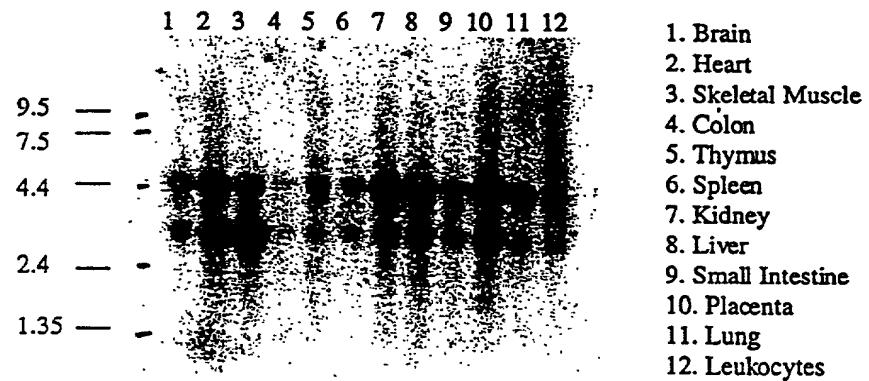


FIG. 6 M

Gene 608



Gene 611

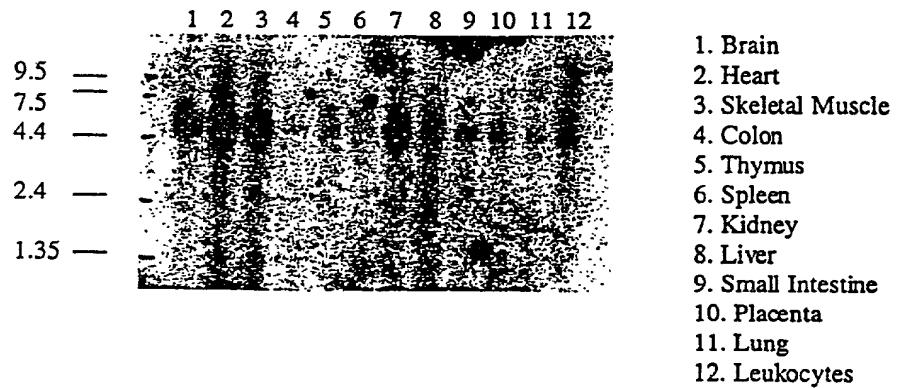
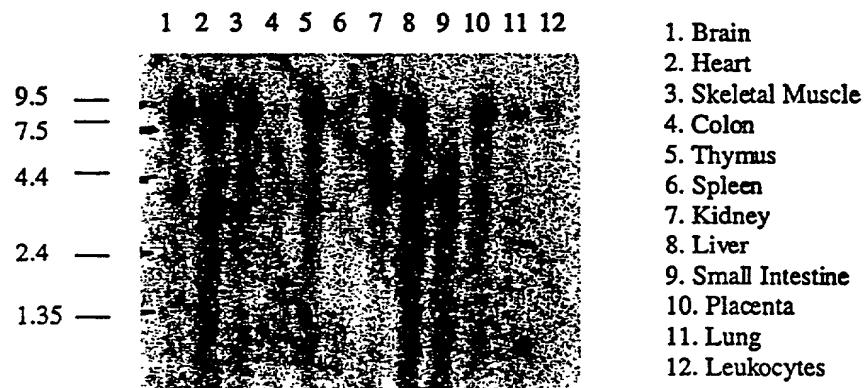


FIG. 6 N

Gene 615



Gene 617

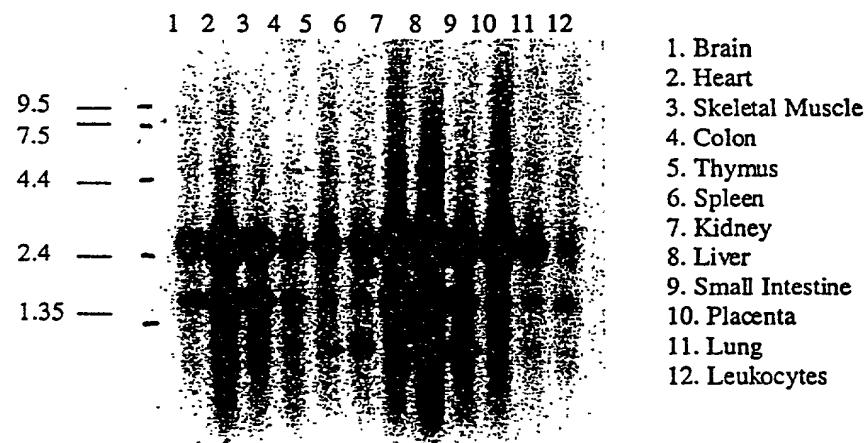
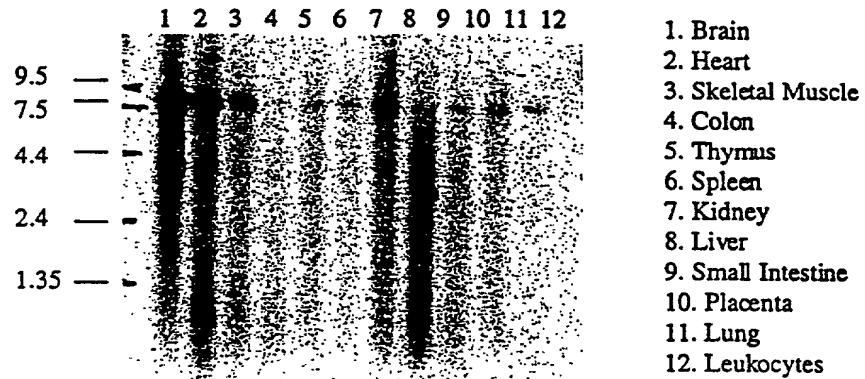


FIG. 6 O

Gene 618



Gene 619

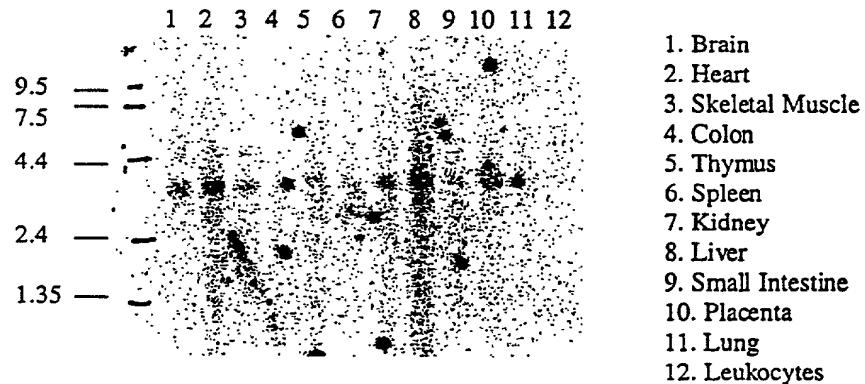
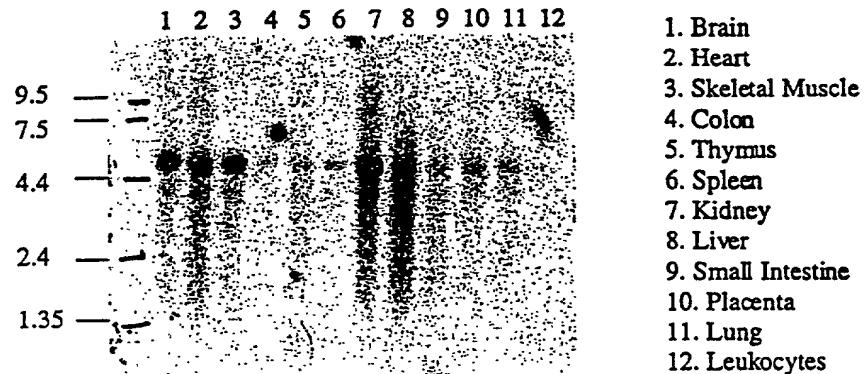


FIG. 6 P

Gene 621



Gene 693

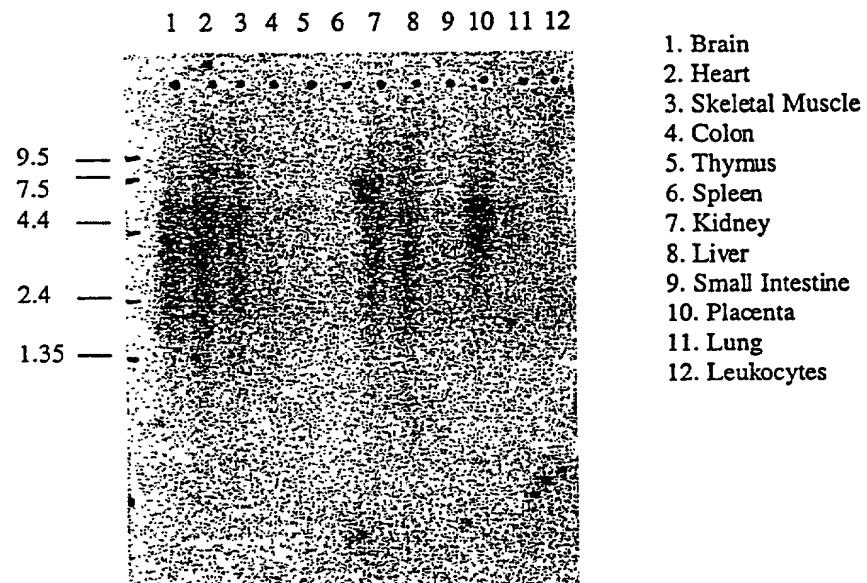
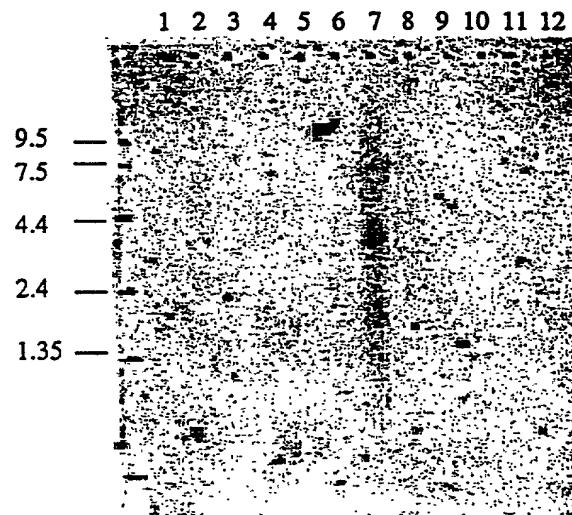


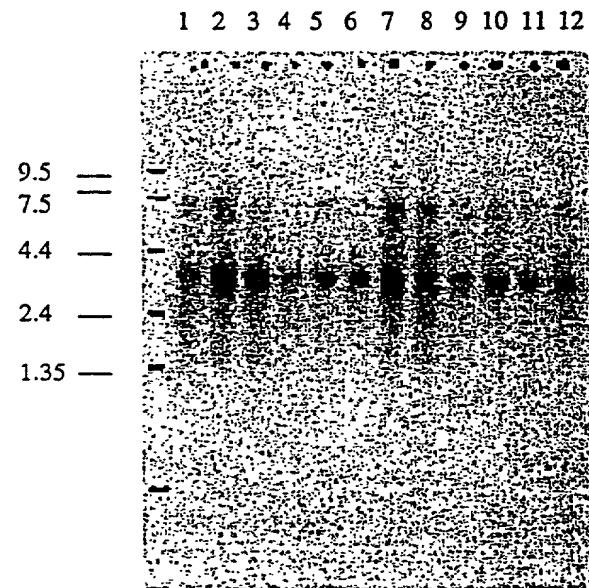
FIG. 6 Q

Gene 698



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

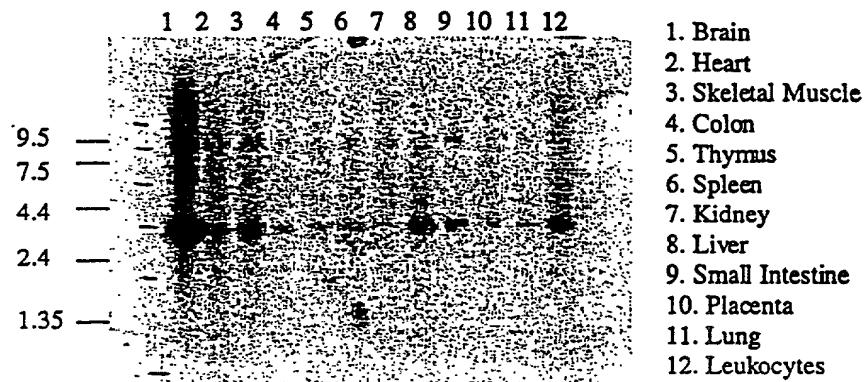
Gene 699



1. Brain
2. Heart
3. Skeletal Muscle
4. Colon
5. Thymus
6. Spleen
7. Kidney
8. Liver
9. Small Intestine
10. Placenta
11. Lung
12. Leukocytes

FIG. 6 R

Gene 702



Gene 722

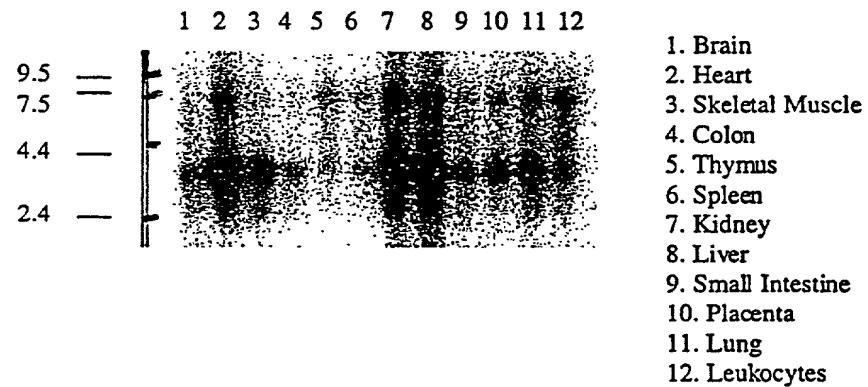
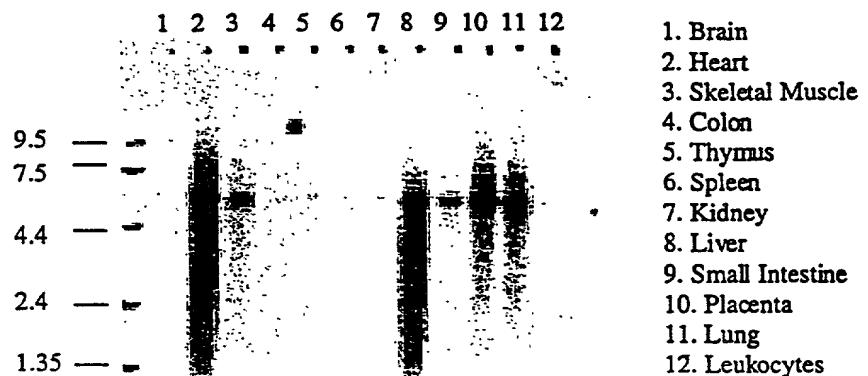


FIG. 6 S

Gene 751



Gene 756

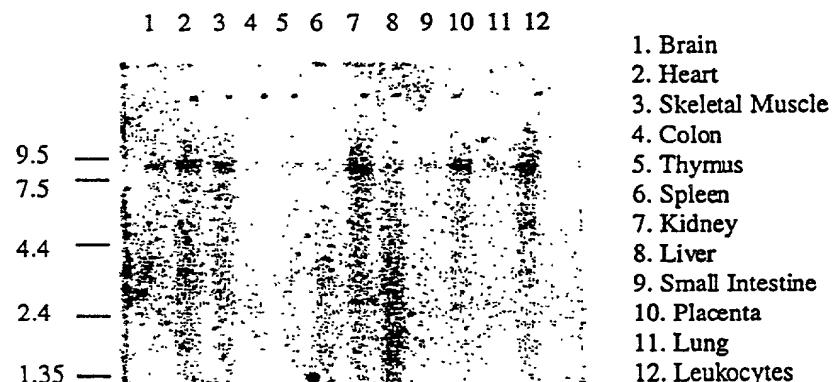
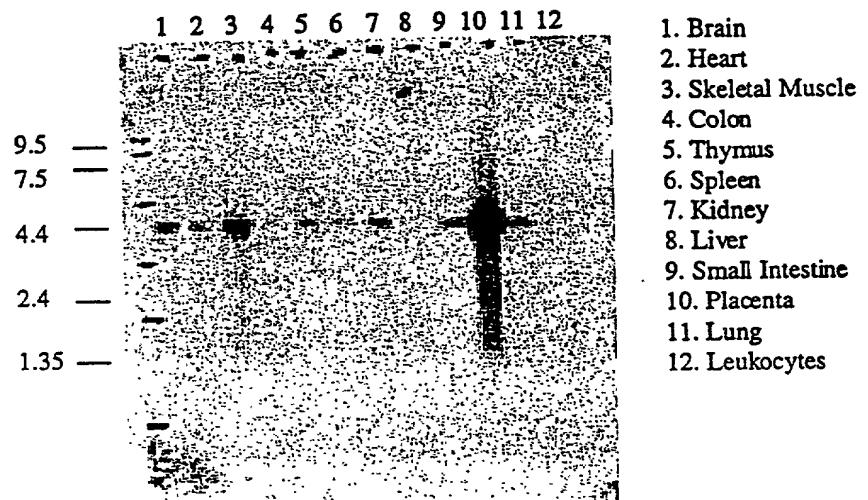


FIG. 6 T

Gene 757



Gene 848

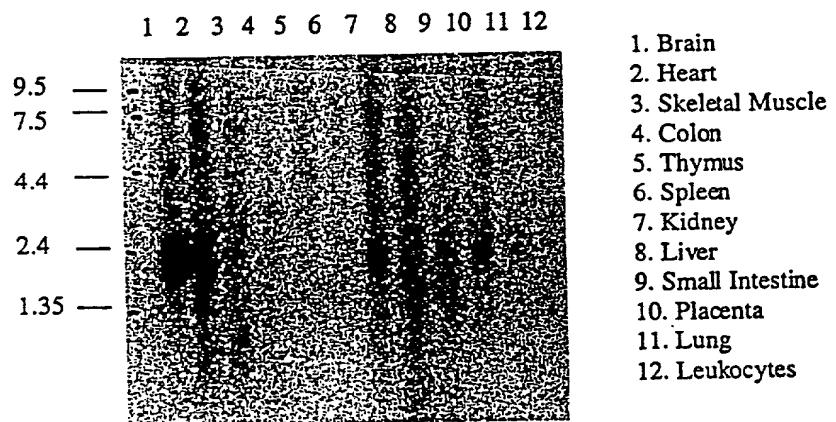


FIG. 6 U

10 30 50

GCTTGCTGTGGCCCTGTCAGGAAGAGTAGAGCTCTGGTCCAGCTCCGCAGGGAGGGAG

70 90 110

GCTGTCACCATGCCGGCCTGCTGCAGCTGCAGTGATGTTTCAGTATGAGACCAACAAA
MetProAlaCysCysSerCysSerAspValPheGlnTyrGluThrAsnLys

130 150 170

GTCACTCGGATCCAGAGCATGAATTATGGCACCATTAAGTGGTTCTTCCACGTGATCATC
ValThrArgIleGlnSerMetAsnTyrGlyThrIleLysTrpPhePheHisValIleIle

190 210 230

TTTCCTACGTTGCTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTC
PheSerTyrValCysPheAlaLeuValSerAspLysLeuTyrGlnArgLysGluProVal

250 270 290

ATCAGTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAG
IleSerSerValHisThrLysValLysGlyIleAlaGluValLysGluGluIleValGlu

310 330 350

AATGGAGTGAAGAAGTTGGTGCACAGTGTCTTGACACCGCAGACTACACCTCCCTTG
AsnGlyValLysLysLeuValHisSerValPheAspThrAlaAspTyrThrPheProLeu

370 390 410

CAGGGGAACTCTTCTTCGTGATGACAAACTTCTCAAAACAGAAGGCCAAGAGCAGCGG
GlnGlyAsnSerPhePheValMetThrAsnPheLeuLysThrGluGlyGlnGluGlnArg

430 450 470

TTGTGTCCCGAGTATCCCACCCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAG
LeuCysProGluTyrProThrArgArgThrLeuCysSerSerAspArgGlyCysLysLys

490 510 530

GGATGGATGGACCCGCAGAGCAAAGGAATTAGACCCGGAGGTGTAGTGCATGAAGGG
GlyTrpMetAspProGlnSerLysGlyIleGlnThrGlyArgCysValValHisGluGly

550 570 590

FIG. 7 A

AACCAGAAGACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGAAAGAGGCC
AsnGlnLysThrCysGluValSerAlaTrpCysProIleGluAlaValGluAlaPro

610

630

650

CGGCCTGCTCTCTGAACAGTGCCGAAAACTTCACTGTGCTCATCAAGAACAAATATCGAC
ArgProAlaLeuLeuAsnSerAlaGluAsnPheThrValLeuIleLysAsnAsnIleAsp

670

690

710

TTCCCCGGCCACAACTACACCACGAGAAACATCCTGCCAGGTTAACATCACTTGAC
PheProGlyHisAsnTyrThrThrArgAsnIleLeuProGlyLeuAsnIleThrCysThr

730

750

770

TTCCACAAGACTCAGAATCCACAGTGTCCTTCCGACTAGGAGACATCTCCGAGAA
PheHisLysThrGlnAsnProGlnCysProIlePheArgLeuGlyAspIlePheArgGlu

790

810

830

ACAGGCGATAATTTTCAGATGTGGCAATTCAGGGCGGAATAATGGCATTGAGATCTAC
ThrGlyAspAsnPheSerAspValAlaIleGlnGlyGlyIleMetGlyIleGluIleTyr

850

870

890

TGGGACTGCAACCTAGACCGTTGGTCCATCATGCCGTCCCAAATACAGTTCCGTCGC
TrpAspCysAsnLeuAspArgTrpPheHisHisCysArgProLysTyrSerPheArgArg

910

930

950

CTTGACGACAAGACCACCAACGTGTCTTGTACCCCTGGCTACAACTTCAGATACGCCAAG
LeuAspAspLysThrThrAsnValSerLeuTyrProGlyTyrAsnPheArgTyrAlaLys

970

990

1010

TACTACAAGGAAACAATGTTGAGAAACGGACTCTGATAAAAGTCTCGGGATCCGTTT
TyrTyrLysGluAsnAsnValGluLysArgThrLeuIleLysValPheGlyIleArgPhe

1030

1050

1070

GACATCCTGGTTTGGCACCGGAGGAAATTGACATTATCCAGCTGGTTGTGTACATC
AspIleLeuValPheGlyThrGlyLysPheAspIleIleGlnLeuValValTyrIle

1090

1110

1130

GGCTCAACCCTCTCCTACTTCGGTCTGGCCACTGTGTTCATCGACTCCTCATCGACACT
GlySerThrLeuSerTyrPheGlyLeuAlaThrValPheIleAspPheLeuIleAspThr

FIG. 7 B

1150 1170 1190
 TACTCCAGTA~~CTGCTGCTCCC~~ATATTATCCCTGGTGC~~AAGTGCTGT~~CAGCCCTGT
 TyrSerSerAsnCysCysArgSerHisIleTyrProTrpCysLysCysCysGlnProCys

1210 1230 1250
 GTGGTCAACGAATACTACTACAGGAAGAAGTGC~~GAGTC~~CATTGTGGAGCCAAGGCCGACA
 ValValAsnGluTyrTyrArgLysLysCysGluSerIleValGluProLysProThr

1270 1290 1310
 TTAAAGTATGTGCCTTGTGGATGAATCCCACATTAGGATGGTGAACCAGCAGCTACTA
 LeuLysTyrValSerPheValAspGluSerHisIleArgMetValAsnGlnGlnLeuLeu

1330 1350 1370
 GGGAGAA~~GTTGCAAGATGTCAAGGGCCAAGAAGTCCC~~AAAGACCTGCGATGGACTTCACA
 GlyArgSerLeuGlnAspValLysGlyGlnGluValProArgProAlaMetAspPheThr

1390 1410 1430
 GATTTGTCCAGGCTGCCCTGGCCCTCCATGACACACCCCCGATTCTGGACAAACCAGAG
 AspLeuSerArgLeuProLeuAlaLeuHisAspThrProProIleProGlyGlnProGlu

1450 1470 1490
 GAGATAACAGTGCTTAGAAAGGAGGCCACTCTAGATCCAGGGATAGCCCCGTCTGGTGC
 GluIleGlnLeuLeuArgLysGluAlaThrProArgSerArgAspSerProValTrpCys

1510 1530 1550
 CAGTGTGGAAAGATGCCTCCCATCTCAACTCCCTGAGAGCCACAGGTGCCTGGAGGAGCTG
 GlnCysGlyArgCysLeuProSerGlnLeuProGluSerHisArgCysLeuGluLeu

1570 1590 1610
 TGCTGCCGGAAAAAGCCGGGGCCTGCATCACCACCCTCAGAGCTGTCAGGAAGCTGGTC
 CysCysArgLysProGlyAlaCysIleThrSerGluLeuPheArgLysLeuVal

1630 1650 1670
 CTGTCCAGACACGTCCTCGCAGTTCCCTCCTGCTCTACCAGGAGCCCTTGCTGGCGCTGGAT
 LeuSerArgHisValLeuGlnPheLeuLeuTyrGlnGluProLeuLeuAlaLeuAsp

1690 1710 1730

FIG. 7 C

GTGGATTCCACCAACAGCCGGCTGCCGCAGTGCTACAGGTGCTACGCCACCTGGCGC
ValAspSerThrAsnSerArgLeuArgHisCysAlaTyrArgCysTyrAlaThrTrpArg

1750

1770

1790

TTCGGCTCCCAGGACATGGCTGACTTGCCATCCTGCCAGCTGCTGCCGCTGGAGGATC
PheGlySerGlnAspMetAlaAspPheAlaIleLeuProSerCysCysArgTrpArgIle

1810

1830

1850

CGGAAAGAGTTCCAAAGAGTGAAGGGCAGTACAGTGGCTTAAGAGTCCTTACTGAAGC
ArgLysGluPheProLysSerGluGlyGlnTyrSerGlyPheLysSerProTyrEnd

1870

1890

1910

CAGGCACCGTGGCTACGTCTGTAATCCCAGCGCTTGGGAGGCCGAGGCAGGCAGATCA

1930

1950

1970

CCTGAGATCGGGAGTTGGAGACCCGCCTGGCTAACAAAGGCGAAATCCTGTCTGTACTAAA

1990

2010

2030

AATACAAAATCAGCCAGACATGGTGGCATGCACCTGCAATCCCAGCTACTCGGGAGGCT

2050

2070

2090

GAGGCACAAGAATCATGAACCCGGGAGGCAGAGGTTGTAGTGAGGCCAGATTGTGCCA

2110

2130

2150

CTGCTCTCCAGCCTGGGAGGCACAGCAAACTGTCCCCAAAAAAAAGAGTCCTTAC

2170

2190

2210

CAATAGCAGGGGCTGCAGTAGCCATGTTAACATGACATTACCAGCAACTGAACTTCAC

2230

2250

2270

CTGCAAAGCTCTGTGGCCACATTTCAGCCAAAGGAAATATGCTTCATCTTCTGTTGC

2290

2310

2330

TCTCTGTGTCTGAGAGCAAAGTGACCTGGTTAAACAACCAGAATCCCTCTACATGGACT

2350

2370

2390

FIG. 7 D

CAGAGAAAAGAGATTGAGATGTAAGTCTCAACTCTGTCCCCAGGAAGTTGTGTGACCCCTA

2410

2430

2450

GGCCTCTCACCTCTGTGCCTCTGTCTCCTTGTGCCAACTACTATCTCAGAGATATTGT

2470

2490

2510

GAGGACAAATTGAGACAGTCACATGAACGTCTTTAATGTGTAAAGATCTACATGAAT

2530

2550

2570

GCAAAACATTCATTATGAGGTAGACTAGGATAATGTCCAACAAAAACAAACCCTTT

2590

2610

2630

CATCCTGGCTGGAGAACATGGAGAACCTAAAGGTGGCCACAAATTCTTGACACTCAAGTC

2650

2670

2690

CCCCAAGACCTAAGGTTTATCTCCTCCCCTGAATATGGTGGCTCTGATTGCTTAT

2710

2730

2750

CCAAAAGTGGAGTGACATTGTGTCAGTTCACTCCTGATCTTAAGAGGCTGACAGCTT

2770

2790

2810

CTACTTGCTGTCCCTTGGAACTCTTGCTATCGGGGAAGCCAGACGCCATTAAAAGTCTG

2830

2850

2870

CCTATCCTGGCCAGGTGTGGCTCACACCTGTAATCCAGCACTTGGGAGACCAAGG

2890

2910

2930

CGGGCGGATCACTAAAGTCAGGAGTCCAAGACCAAGACTCGCCAACATGGTAAACCGTA

2950

2970

2990

TCTCTAATAAAAATACAAAATTAGCTGGCATGGTGCAGGCACCTGTAGTCCTAGCTAT

3010

3030

3050

CAAGAGGCTGAGACAGGAGAACACTTGAACCTGGGAGGTTGCATTGAGCTGAG

FIG. 7 E

3070 3090 3110
ATCGTGCCACTGCACCCAGGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAAAAAA

3130 3150 3170
AAAAAGAAAAAAAATGTCTGCCTATCCTGAGACTGCCCTGCTGTGAGGAAGCCCCAAGCA

3190 3210 3230
GTCACGTGGACAGTGCCTGACCAGCCCCAGCTTCAAGCCATCCAAGCCCAGTCACCAA

3250 3270 3290
CATGAGAGAGAAGAAGCCTTCAGGTGATTCTGGACTCCACTAACATATGACTGATAACGC

3310 3330 3350
ATGATAACATCCAAAGTGAGAACTGCCCATAAATCCAGAAAACCACATTGCTATCTTAAG

3370 3390 3410
TCCCTAACGTTGGGCTTATTGTTCCACAGCAACAGGTAACGGAACAGAGGGCAAGCC

3430 3450 3470
TGATGAATGGCACACAGACTCAGCCATACCTCCCTGGTCTAACGTTCTCAGGGAGC

3490 3510 3530
CCGGACCAACCTGGAGCCTCAGGAACCTAGGTTCCACTGGACAGTTCTAGAAGGGCT

3550 3570 3590
ATAGACCAAATCAGGTAACTCACCAGACCAGCCTGGAATCTATCAAATCTAACTGCTGA

3610 3630 3650
GCTACCCAGTGCATTCCGATCCTCATCACAAATTCTTGACTGAAGGCCGGCGTGGTGGC

3670 3690 3710
TCACGCCTGTAATCCCAGCACTTGGGAGGCTGAGGCAGGTGGATCACCTGAGGTAGGA

FIG. 7 F

3730 3750 3770
GTTCGAGACCAGCCTGGCCAACATGGTGAGACCCCTGTCTACTAAGAAATACAAAAATTAA

3790 3810 3830
GGTGGGGTGGCGGTGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAAC

3850 3870 3890
TCTTGAACCTGGAAGGTGGAGGTTGCAATAAGCCGAGATAGTGCCACTGCACTCCAGCCT

3910 3930 3950
AGATAACAGAGCAAGACTCTGTCTAAAAAACAAACAACAACAACAAAACAATTCTAT

3970 3990 4010
GACTGAAAGTGAATAAGCTGGCTTATGCCATTAAACACTCTGTACTTGCAGCCAAT

4030 4050 4070
CAGAACTGACGCAGTCTGGTGCTAGCTGCTTCAGCAACCCACACCACACTTTACC

4090 4110 4130
ATTCACATCAACTGCTGAGAATATGAAAATGCACAGTGACAGGTTAGGATCCTG

4150 4170 4190
CTTCAGGATTCCCTTCTGGTTGGTCACTAGAGTTGGCTATTATCTGTTCTAAC

4210 4230 4250
AATAGCTATTTATCGAATAGTTAGAGACCACTATTAATATTGTGACTGATGAAGGAT

4270 4290 4310
CTGTGAATTTTATATGTTCTAAGAGTTACCATTTGATACCTTTAAAAACCAAGC

4330 4350 4370
AGCTTCTACTATATTGTAACAGCATGAATAAACCACTTTGATACAGGGTT

4390 4410 4430

FIG. 7 G

TATTTGGCTTAAACTCAGGAACCAAGTTAATTATGCCAGATTGAACTTGATTTACT

4450

4470

4490

ACCTTTCAAAGATATTAAAAAGTGGATTACTACATATGATTCTTGAGCTTACAT

4510

4530

4550

TTCTTACTCACGAATTCTATGTCACTGTTACAAGTTCCATTCTGATGGCTCTGGC

4570

4590

4610

CTTGTACCTTGGTGCCTTATTCTAGTATGTTCTATCACCTTAATGAGGCC

4630

4650

4670

GCAGATGGAGTCAGAATGTGAAATTACAAATAATCACTGGATCCATCTACTGTTCCAT

4690

4710

4730

CACCTCCCCACTGATGCTCTGGCGAGAGAGTGTGTCACCTCAACTGTGTGTAATA

4750

4770

4790

TGTCAGACACGTCTACAATAACAGGCGTCATATTGTATTATTTAGTTACTGTAGA

4810

4830

4850

AAATAATGTCACCGCCAAAGGTGATGAGAGTCACGTTTAGGATCTGTTCTTAC

4870

4890

4910

TTAAAGACAGACTTCTGCTACGGTAATTGCCAGTATTGATGGCTTCTGTGTCAGA

4930

4950

4970

AGAGAAGGGATCTGTTCTTGGCTGATTTCACATAGCATTGGTAATAGACATGCATT

4990

5010

5030

TCTTTCTAAAGGGAGTAACTTTAAACCCCTGATTTAGCCTGGCAATGTAAG

5050

5070

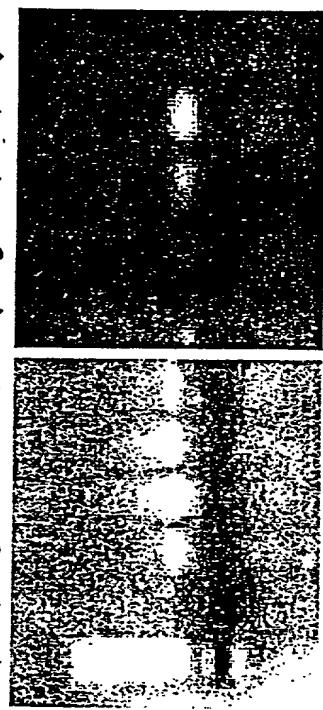
TGTCCTTAATGTGACTGTTGATAATTAAAAAGGTATATAATT

FIG. 7 H

FIG. 8

RT/PCR of Gene561.nt1 and Gene561.nt2

Gene561.nt1 Gene561.nt2



Marker
Primers Only
Spleen
Thymus
Lung
Brain
Thymus
Lung
Spleen
Primers Only

Marker
Primers Only
Spleen
Thymus
Lung
Brain
Thymus
Lung
Spleen
Primers Only

10 30 50

TCGAAACAGCTGCCGGCTGGTCCCAGGCCGAGGCCGGCGCAGGGAGGGAGGAGCCGCCGG

70 90 110

GCTGTGGGGCGCCGCGAGCTGGGCCGGCTCGGTGTGCCCGCGCCAGCCCGCTCCA

130 150 170

GACGCGCACCTGGCGCTCCAAGAAGAGGCCGAAGTTGCCGCAGCCGTGAGTTGGAGC

190 210 230

TCGCGCCGGGCCGCTGCGCCGGAGCTCCGGGGCTTCCTCGCTCCGGTATTGTTG

250 270 290

CAAACTTGCTGCTCTCCGCCGCGGCCCAACTCGGCCGACGCCGGCGAGAGCCG

310 330 350

AGCCGGGGCGCTGTGCGCAGCGCTCGGCCAGGCCGGCGGGCATGGCGGGGCCGA

370 390 410

GCAGGGGTGGAGAGCCGGGCCAGCAGCAGCCCCTGCCCGGAGCCGGCGCTGAGGGG

430 450 470

CGCGGAGCTCCCGCGAGGACACGTCCAACGCCAGCATGCAGCGCCGGCCCCGCCTG
MetGlnArgProGlyProArgLeu

490 510 530

TGGCTGGTCTGCAGGTGATGGGCTCGTGCGCCGCATCAGCTCCATGGACATGGAGCGC
TrpLeuValLeuGlnValMetGlySerCysAlaAlaIleSerSerMetAspMetGluArg

550 570 590

CCGGGCGACGGCAAATGCCAGCCCATCGAGATCCGATGTGCAAGGACATCGGCTACAAC
ProGlyAspGlyLysCysGlnProIleGluIleProMetCysLysAspIleGlyTyrAsn

610 630 650

FIG. 9 A

ATGACTCGTATGCCAACCTGATGGGCCACGAGAACCGCGCAGGCATCCAGTTG
MetThrArgMetProAsnLeuMetGlyHisGluAsnGlnArgGluAlaAlaIleGlnLeu

670

690

710

CACGAGTTCGCGCCGCTGGTGGAGTACGGCTGCCACGGCCACCTCCGCTTCTTCCTGTGC
HisGluPheAlaProLeuValGluTyrGlyCysHisGlyHisLeuArgPhePheLeuCys

730

750

770

TCGCTGTACCGCGCCGATGTGCACCGAGCAGGTCTCTACCCCCATCCCGCCTGCCGGTCA
SerLeuTyrAlaProMetCysThrGluGlnValSerThrProIleProAlaCysArgVal

790

810

830

ATGTGCGAGCAGGCCCGCTCAAGTGCTCCCCGATTATGGAGCAGTTCAACTTCAAGTGG
MetCysGluGlnAlaArgLeuLysCysSerProIleMetGluGlnPheAsnPheLysTrp

850

870

890

CCCGACTCCCTGGACTGCCGGAAACTCCCCAACAAAGAACGACCCAACTACCTGTGCATG
ProAspSerLeuAspCysArgLysLeuProAsnLysAsnAspProAsnTyrLeuCysMet

910

930

950

GAGGCGCCAACAACGGCTCGGACGGCCCACCCGGGGCTGGGCCTGTTCCGCCGCTG
GluAlaProAsnAsnGlySerAspGluProThrArgGlySerGlyLeuPheProProLeu

970

990

1010

TTCCGGCCGAGCGGCCACAGCGCCAGGAGCACCCGCTGAAGGACGGGGCCCCGGG
PheArgProGlnArgProHisSerAlaGlnGluHisProLeuLysAspGlyGlyProGly

1030

1050

1070

CGCGGGCGCTGCGACAACCCGGCAAGTTCCACCACGTGGAGAAGAGCGCGCTGCGCG
ArgGlyGlyCysAspAsnProGlyLysPheHisHisValGluLysSerAlaSerCysAla

1090

1110

1130

CCGCTCTGCACGCCGGCTGGACGTGTACTGGAGCCCGAGGACAAGCGCTTCGAGTG
ProLeuCysThrProGlyValAspValTyrTrpSerArgGluAspLysArgPheAlaVal

1150

1170

1190

FIG. 9 B

GTCTGGCTGGCCATCTGGCGGTGCTGTGCTTCTTCAGCGCCTCACCGTGCTCACC
ValTrpLeuAlaIleTrpAlaValLeuCysPhePheSerSerAlaPheThrValLeuThr

1210

1230

1250

TTCCTCATCGACCCGGCCGCTTCCGCTACCCCGAGCGCCCCATCATCTTCCTCTCCATG
PheLeuIleAspProAlaArgPheArgTyrProGluArgProIleIlePheLeuSerMet

1270

1290

1310

TGCTACTGCGTCTACTCCGTGGCTACCTCATCCGCCTTCGCCGGCGCCGAGAGCATC
CysTyrCysValTyrSerValGlyTyrLeuIleArgLeuPheAlaGlyAlaGluSerIle

1330

1350

1370

GCCTGCGACCGGGACAGCGGCCAGCTCTATGTCATCCAGGAGGGACTGGAGAGCACCGGC
AlaCysAspArgAspSerGlyGlnLeuTyrValIleGlnGluGlyLeuGluSerThrGly

1390

1410

1430

TGCACGCTGGTCTTCCTGGCTACTACTTCGGCATGGCCAGCTCGCTGTGGTGGGTG
CysThrLeuValPheLeuValLeuTyrTyrPheGlyMetAlaSerSerLeuTrpTrpVal

1450

1470

1490

GTCCTCACGCTCACCTGGTTCTGGCCGCCGGCAAGAAGTGGGCCACGAGGCCATCGAA
ValLeuThrLeuThrTrpPheLeuAlaAlaGlyLysLysTrpGlyHisGluAlaIleGlu

1510

1530

1550

GCCAACAGCAGCTACTCCACCTGGCAGCCTGGCCATCCGGCGGTGAAGACCATCCTG
AlaAsnSerSerTyrPheHisLeuAlaAlaTrpAlaIleProAlaValLysThrIleLeu

1570

1590

1610

ATCCTGGTCATGCGCAGGGTGGCGGGGGACGAGCTCACCGGGCTGCTACGTGGGCAGC
IleLeuValMetArgArgValAlaGlyAspGluLeuThrGlyValCysTyrValGlySer

1630

1650

1670

ATGGACGTCAACGCGCTCACCGGCTTCGTGCTCATTCCCTGGCCTGCTACCTGGTCATC
MetAspValAsnAlaLeuThrGlyPheValLeuIleProLeuAlaCysTyrLeuValIle

1690

1710

1730

FIG. 9 C

GGCACGTCTTATCCTCTCGGGCTTCGTGGCCCTGTTCCACATCCGGAGGGTGTGAAG
GlyThrSerPheIleLeuSerGlyPheValAlaLeuPheHisIleArgArgValMetLys

1750

1770

1790

ACGGGCAGGAAACACGGACAAGCTGGAGAAGCTCATGGTGCCTATCGGGCTTCTCT
ThrGlyGlyGluAsnThrAspLysLeuGluLysLeuMetValArgIleGlyLeuPheSer

1810

1830

1850

GTGCTGTACACCGTGCCGCCACCTGTGTGATCGCCTGCTACTTTACGAACGCCCTCAAC
ValLeuTyrThrValProAlaThrCysValIleAlaCysTyrPheTyrGluArgLeuAsn

1870

1890

1910

ATGGATTACTGGAAGATCCTGGCGCGCAGCACAAAGTGCAGAACAAACCAGACTAAA
MetAspTyrTrpLysIleLeuAlaAlaGlnHisLysCysLysMetAsnAsnGlnThrLys

1930

1950

1970

ACGCTGGACTGCCTGATGGCCGCCTCCATCCCCGCCGTGGAGATCTCATGGTGAAGATC
ThrLeuAspCysLeuMetAlaAlaSerIleProAlaValGluIlePheMetValLysIle

1990

2010

2030

TTTATGCTGGTGGTGGGGATCACCAAGCAGGGATGTGGATTTGGACCTCCAAGACTCTG
PheMetLeuLeuValValGlyIleThrSerGlyMetTrpIleTrpThrSerLysThrLeu

2050

2070

2090

CAGTCCTGGCAGCAGGTGTGCAGCGTAGGTTAAAGAAGAAGAGCCGGAGAAACCGGCC
GlnSerTrpGlnGlnValCysSerArgArgLeuLysLysSerArgArgLysProAla

2110

2130

2150

AGCGTGATCACCAAGCGGTGGGATTACAAAAAAAGCCCAGCATCCCCAGAAAATCACCAC
SerValIleThrSerGlyGlyIleTyrLysLysAlaGlnHisProGlnLysThrHisHis

2170

2190

2210

GGGAAATATGAGATCCCTGCCAGTCGCCACCTGCGTGTGAACAGGGCTGGAGGGAGG
GlyLysTyrGluIleProAlaGlnSerProThrCysValEnd

2230

2250

2270

FIG. 9 D

GCACAGGGCGCCCGGAGCTAAGATGTGGTGCTTTCTGGTGTGTTTCTTCT

2290 2310 2330

TCTTCTTTTTTTTATAAAAGCAAAAGAGAAATACATAAAAAGTGTACCTG

2350 2370 2390

AAATTCAAGGATGCTGTGATACTGAAAGGAAAATGTACTAAAGGGTTTGT

2410 2430 2450

TTGGTTTCCAGCGAAGGGAAGCTCCTCCAGTGAAGTAGCCTCTTGTGTAACTAATTG

2470 2490 2510

GGTAAAGTAGTTGATTCAGCCCTCAGAAGAAAACCTTTGTTAGAGCCCTCCSTAAATAT

2530 2550 2570

ACATCTGTGTATTCAGTTGGCTTGTACCCATTACAATAAGAGGACAGATAACTGC

2590 2610 2630

TTTCAAATTCAAGAGCCTCCCTGGTTAACAAATGAGCCATCCCCAGGGCCCACCCCC

2650 2670 2690

AGGAAGGCCACAGTGCTGGCGGCATCCCTGCAGAGGAAAGACAGGACCCGGGGCCCGCC

2710 2730 2750

TCACACCCAGTGGATTGGAGTTGCTTAAATAGACTCCGGCCTTCACCAATAGTCTCT

2770 2790 2810

CTGCAAGACAGAAACCTCCATCAAACCTCACATTGTGAACCTAAACGATGTGCAATACA

2830 2850 2870

TTTTTTCTTCTTGAAAATAAAAGAGAAACAGTATTTGCTATATATAAGACA

2890 2910 2930

FIG. 9 E

ACAAAAGAAATCTCCTAACAAAAGAACTAAGAGGCCAGCCCTCAGAAACCCTTCAGTGC

2950

2970

2990

TACATTTGTGGCTTTAATGGAAACCAAGCCAATGTTATAGACGTTGGACTGATTG

3010

3030

3050

TGGAAAGGAGGGGGGAAGAGGGAGAAGGGATCATTCAAAAGTTACCCAAAGGGCTTATTGA

3070

3090

3110

CTCTTCTATTGTTAACAAATGATTCCACAAACAGATCAGGAAGCACTAGGTTGGCAG

3130

3150

3170

AGACACTTGTCTAGTGATTCTCTCACAGTGCCAGGAAAGAGTGGTTCTGCGTGTGT

3190

3210

3230

ATATTTGTAATATATGATATTTCATGCTCCACTATTTATTAAAAATAAAATATGTTCA

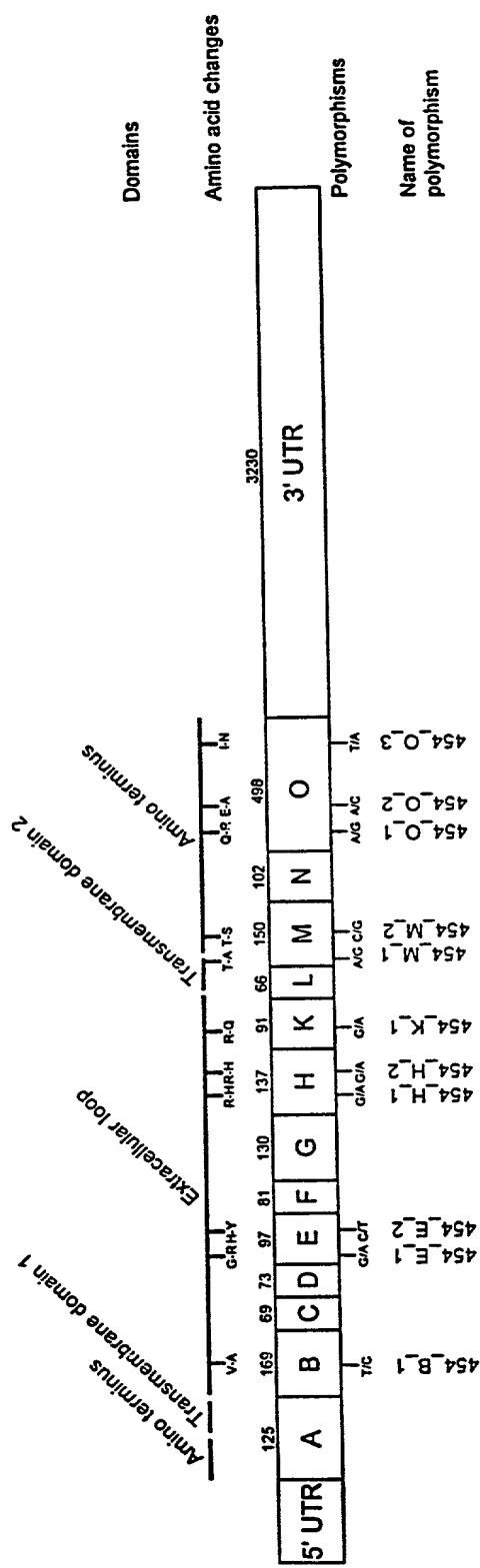
3250

TTTAGTTGCTGCT

FIG. 9 F

FIG. 10

Location of SNPs/Amino Acid Changes/Domain within the Transcript of Gene 454



Chr. 12 Case(Asthma)/Control: Alleles

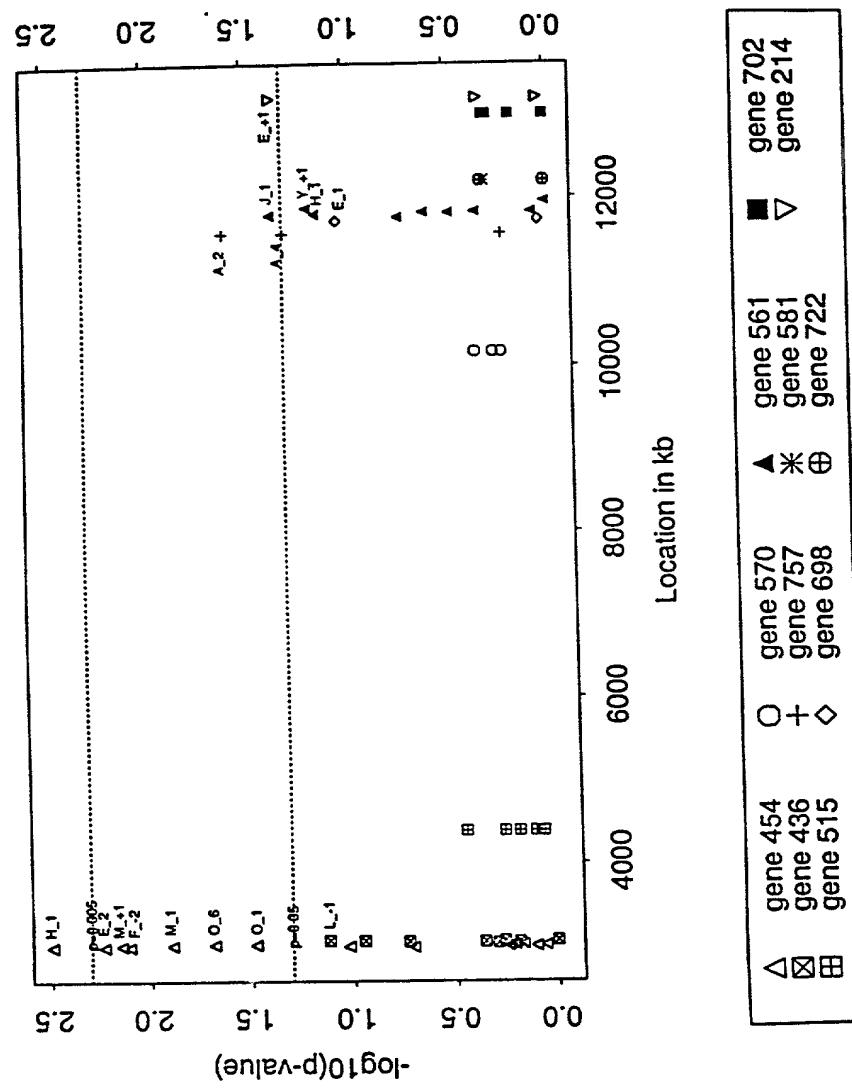
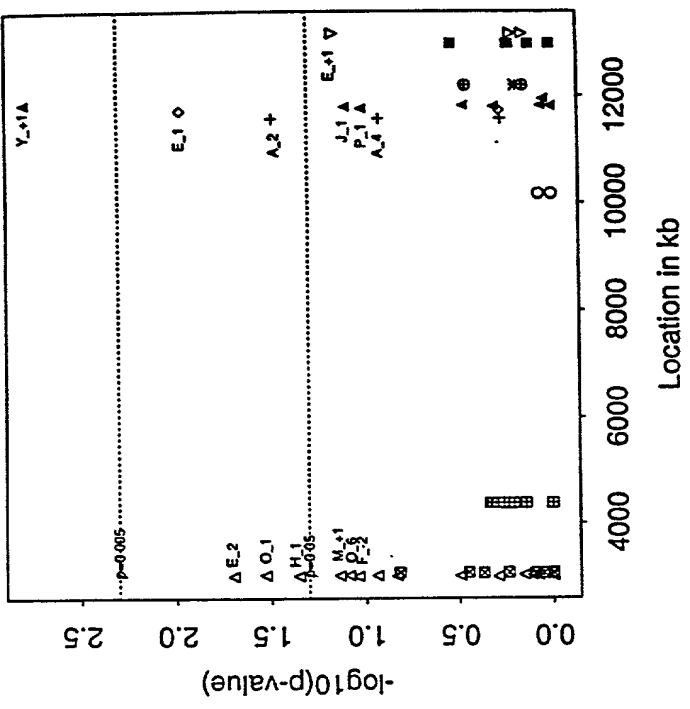
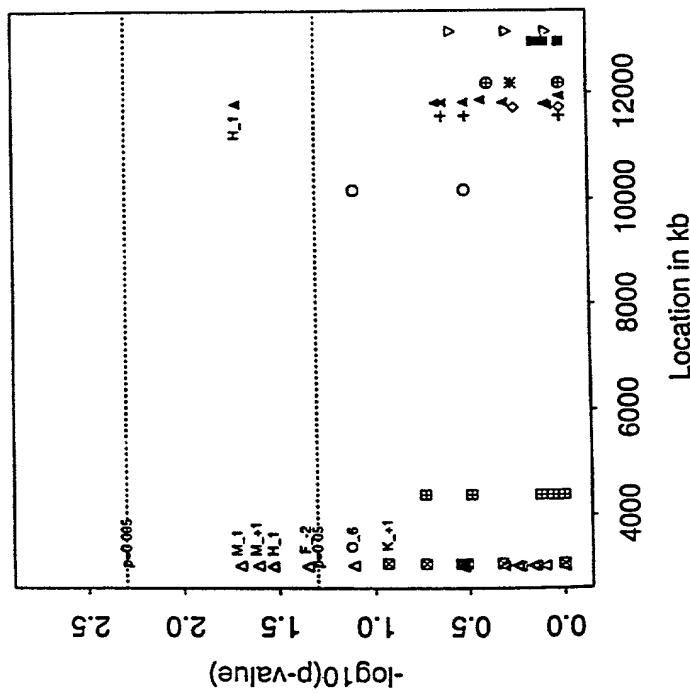


FIG. 1

Chr. 12 Case(Asthma)/Control: Alleles

US

UK



Δ	gene 454
\square	gene 436
\blacksquare	Gene 515
\circ	gene 570
\diamond	gene 436
$*$	gene 577
\oplus	gene 698
\triangledown	Gene 561
\blacksquare	gene 561
\blacksquare	Gene 561
\blacksquare	Gene 722
\blacksquare	Gene 722
\blacksquare	Gene 702
\blacksquare	Gene 214

FIG. 12

Chr. 12 Case(BHR (PC₂₀ <= 16 mg/ml) & Asthma)/Control: Alleles

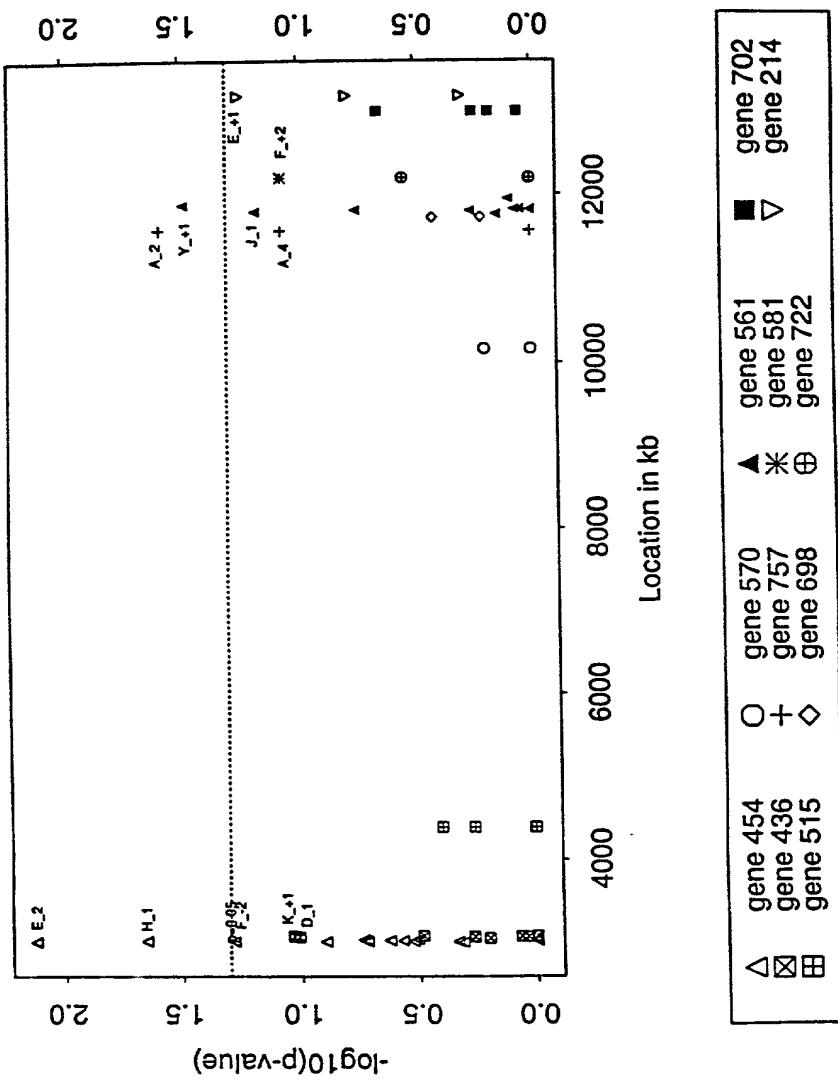


FIG. 13

Chr. 12 Case(BHR (PC₂₀ <= 16 mg/ml) & Asthma)/Control: Alleles

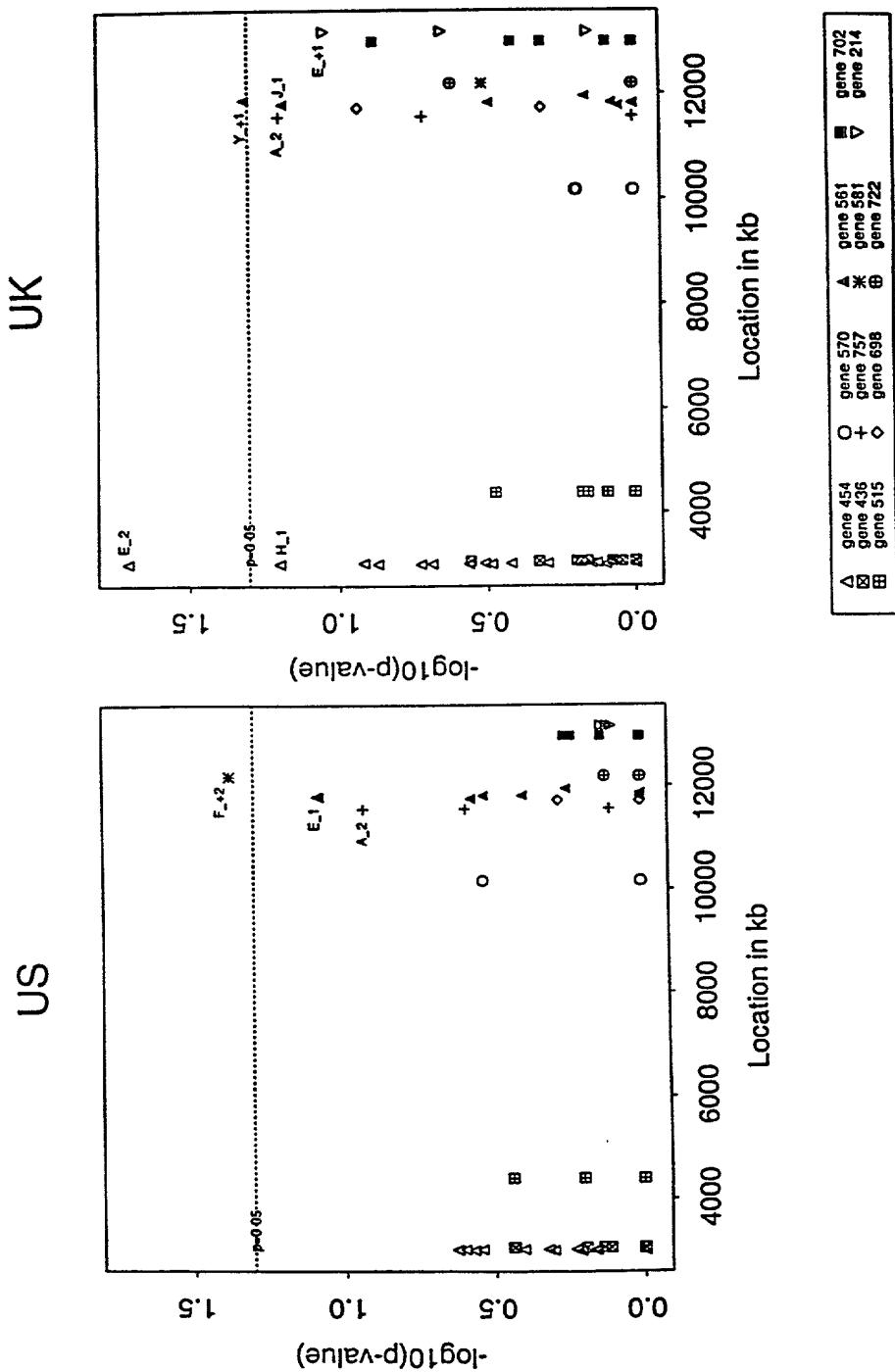


FIG. 14

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

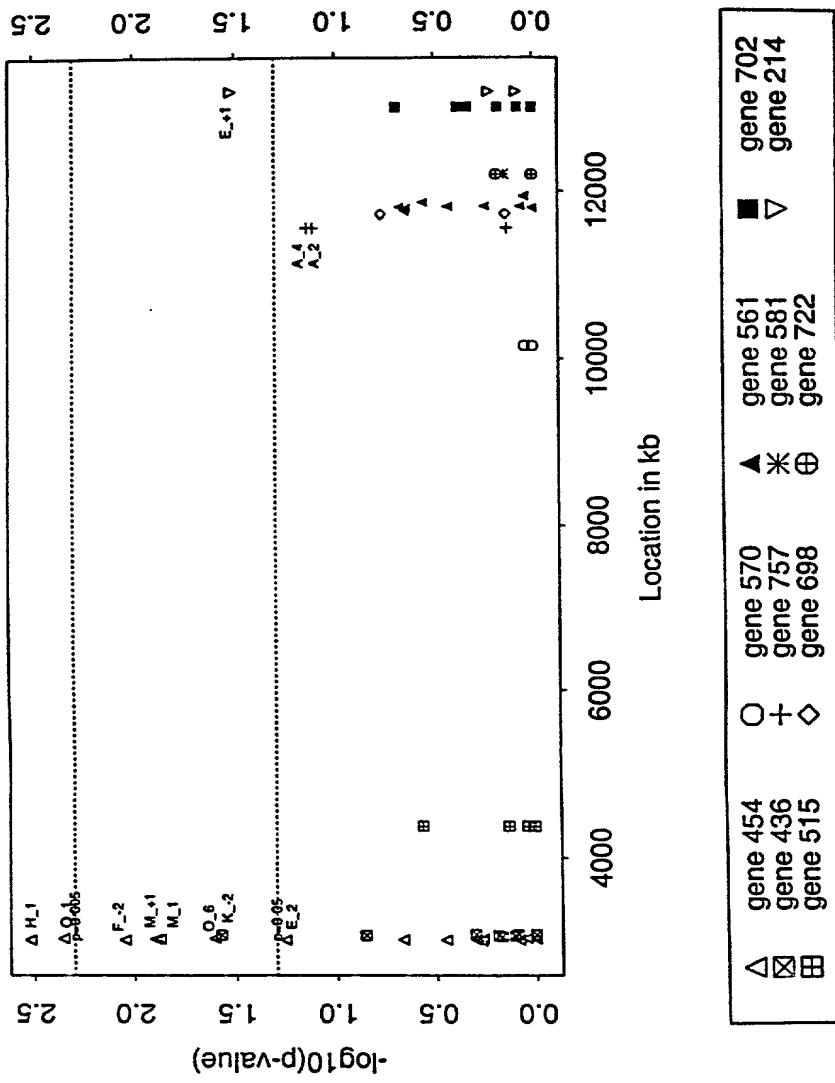


FIG. 15

Chr. 12 Case(Total IgE & Asthma)/Control: Alleles

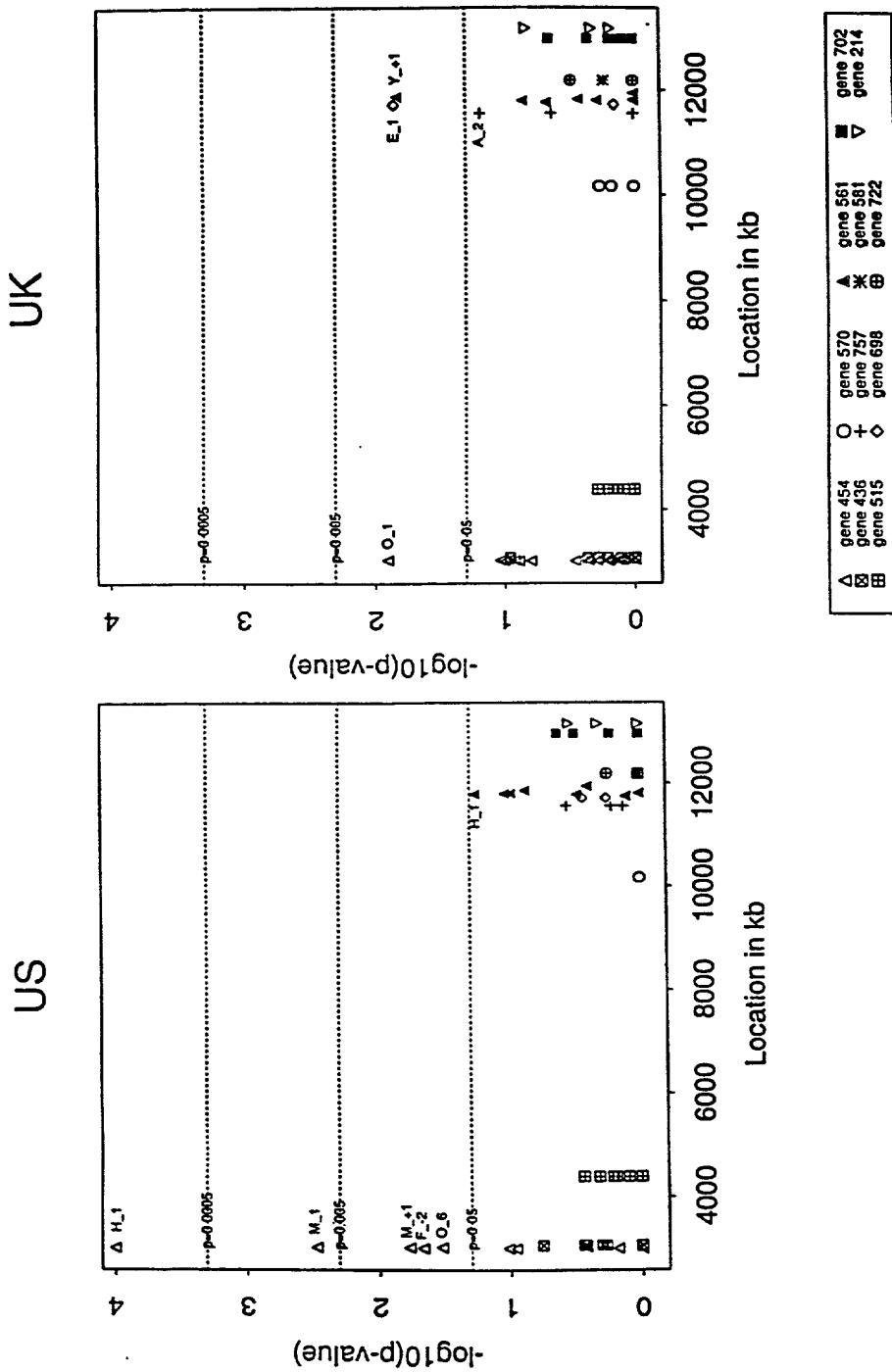


FIG. 16

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

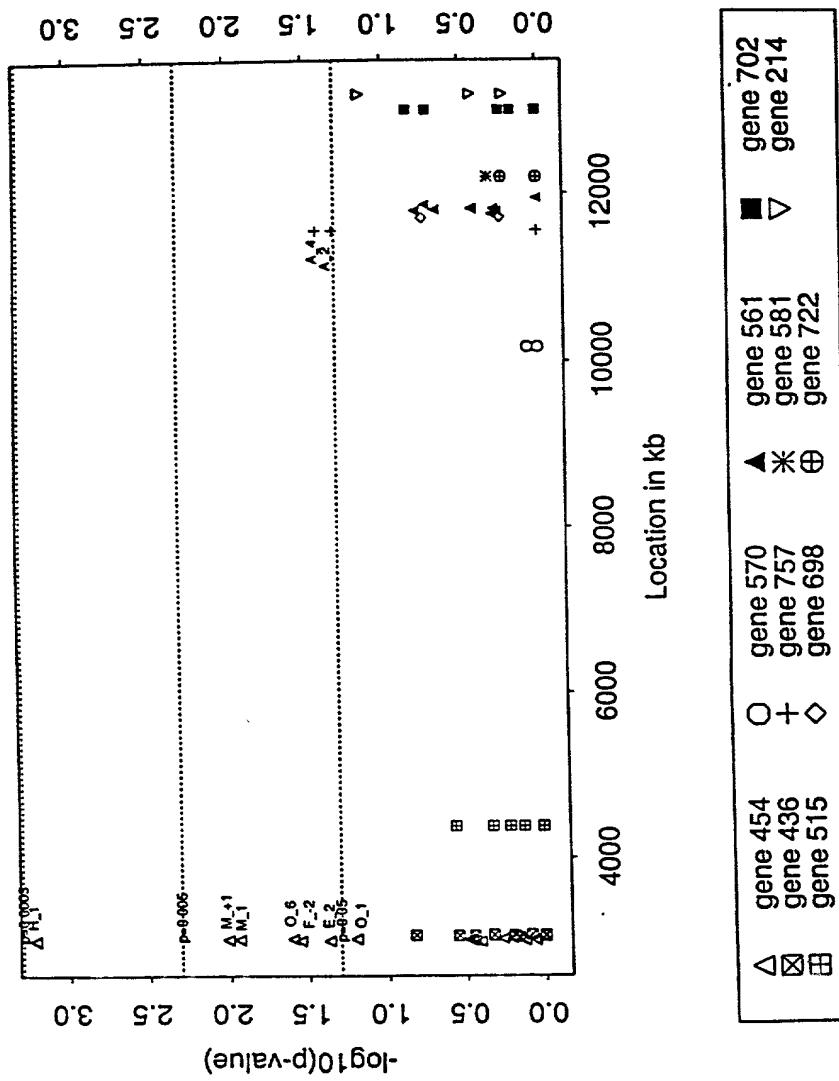


FIG. 17

Chr. 12 Case(Specific IgE & Asthma)/Control: Alleles

US

UK

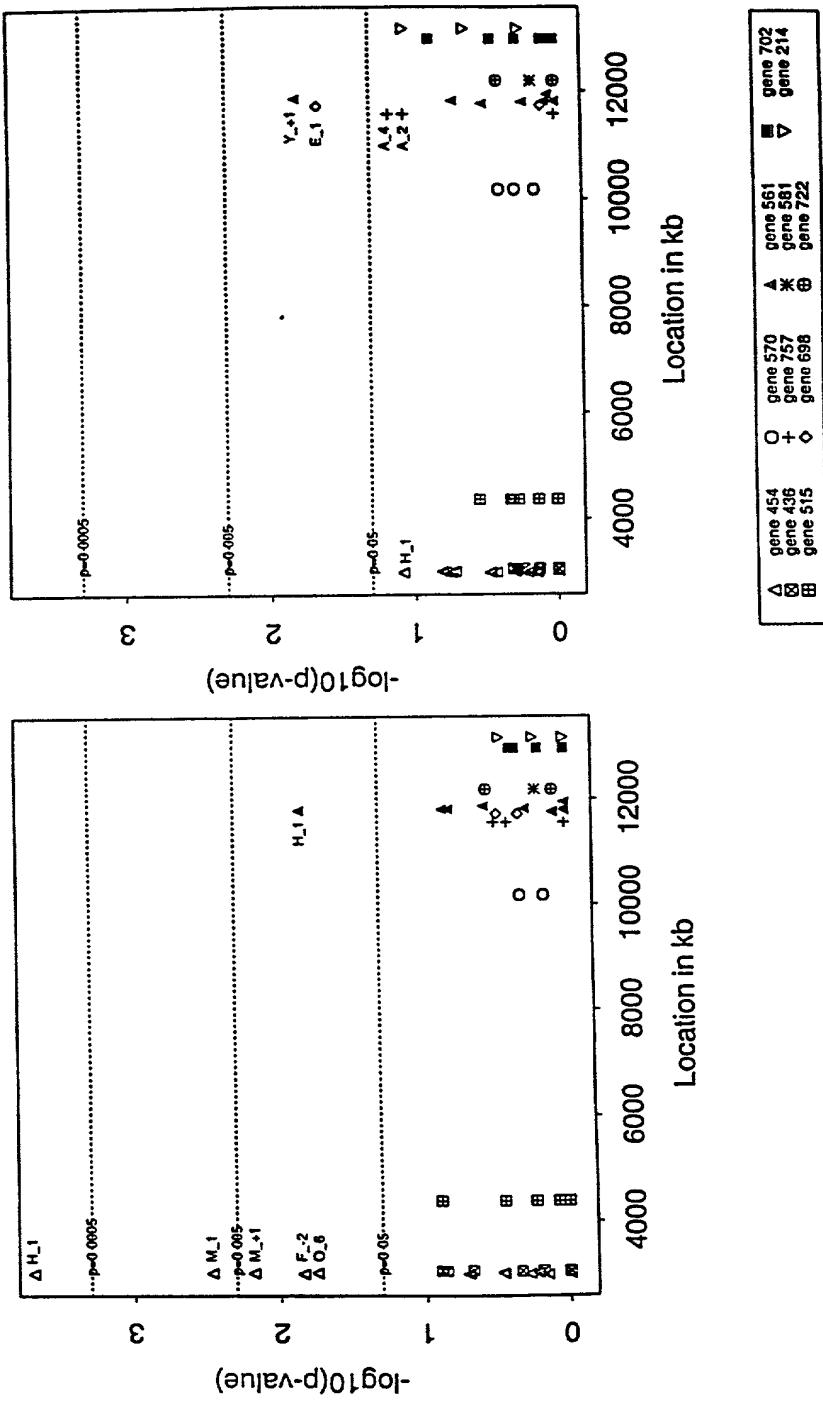


FIG. 18

Chr. 12 Case(Asthma)/Control: Haplotype

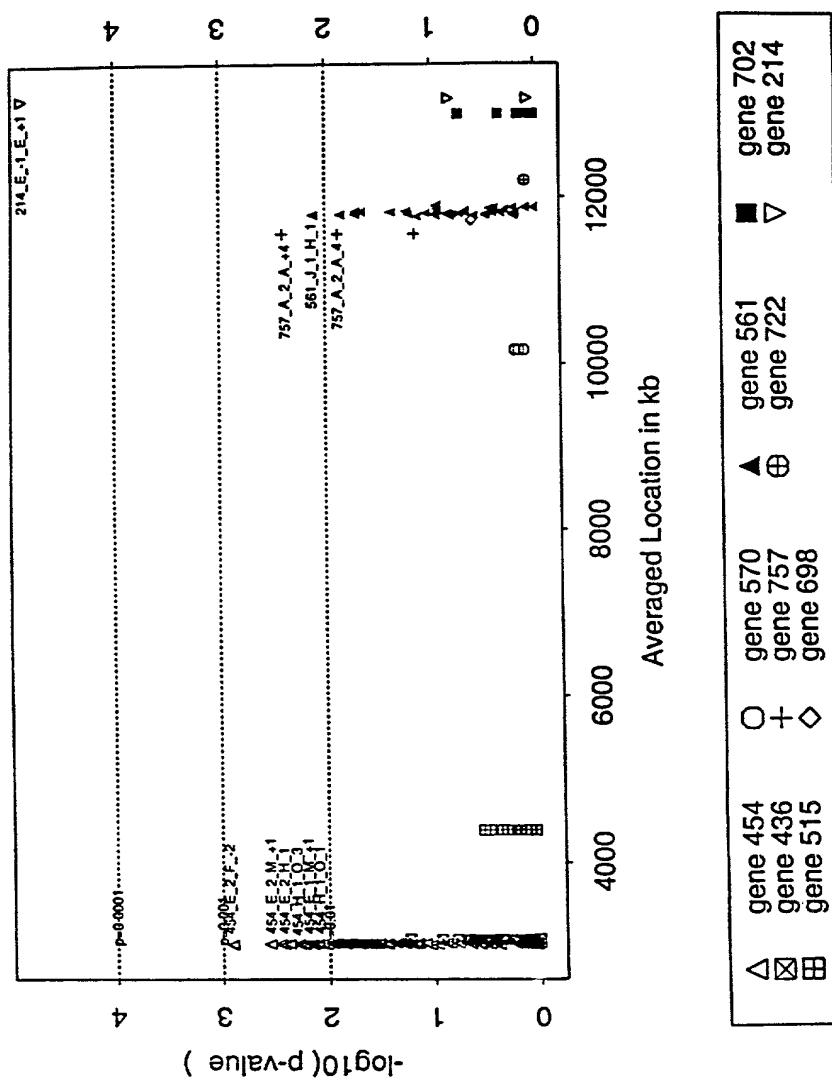


FIG. 19

Chr. 12 Case(Asthma)/Control: Haplotype

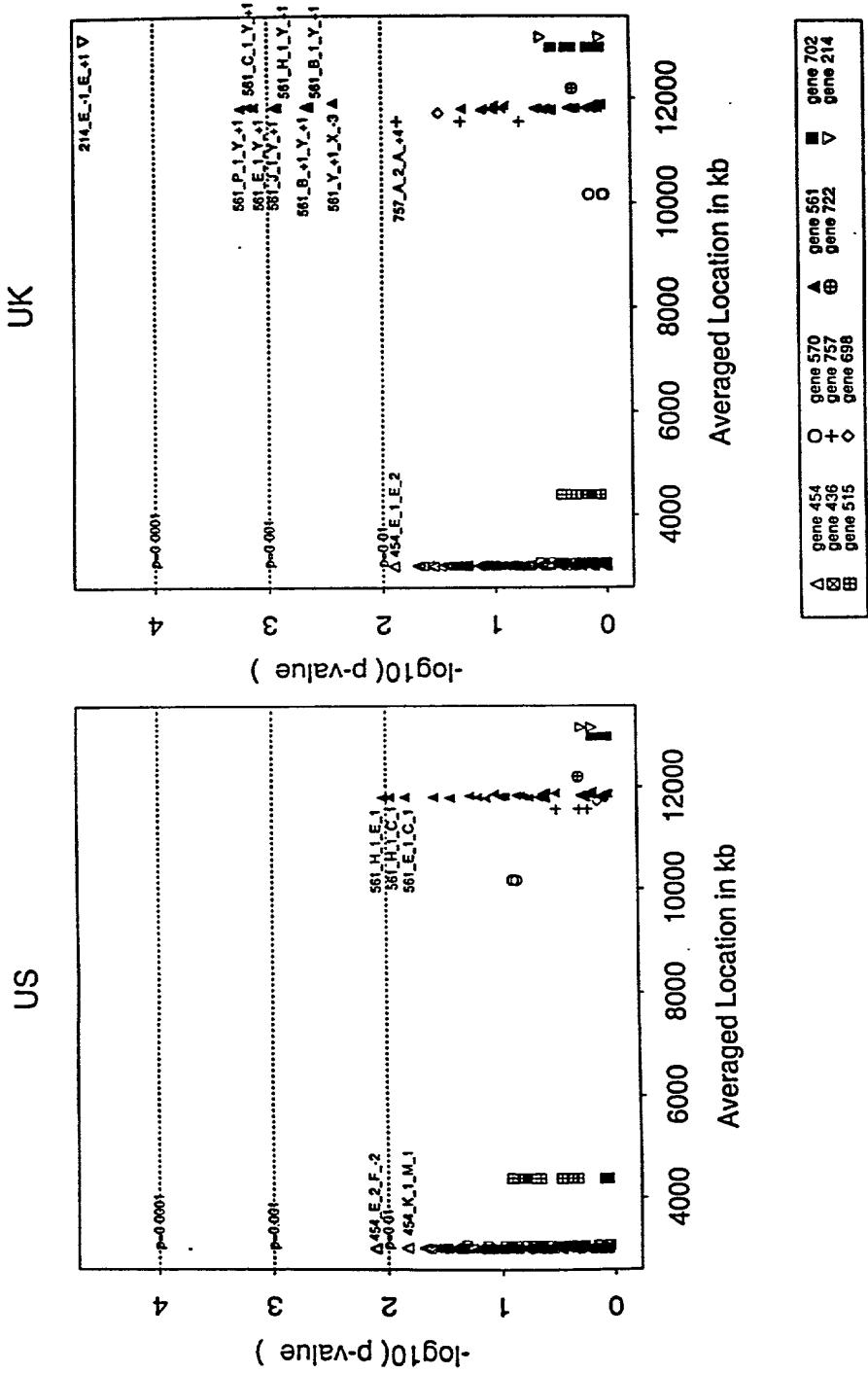


FIG. 20

Chr. 12 Case(BHR (PC₂₀ <= 16 mg/ml) & Asthma)/Control: Haplotype

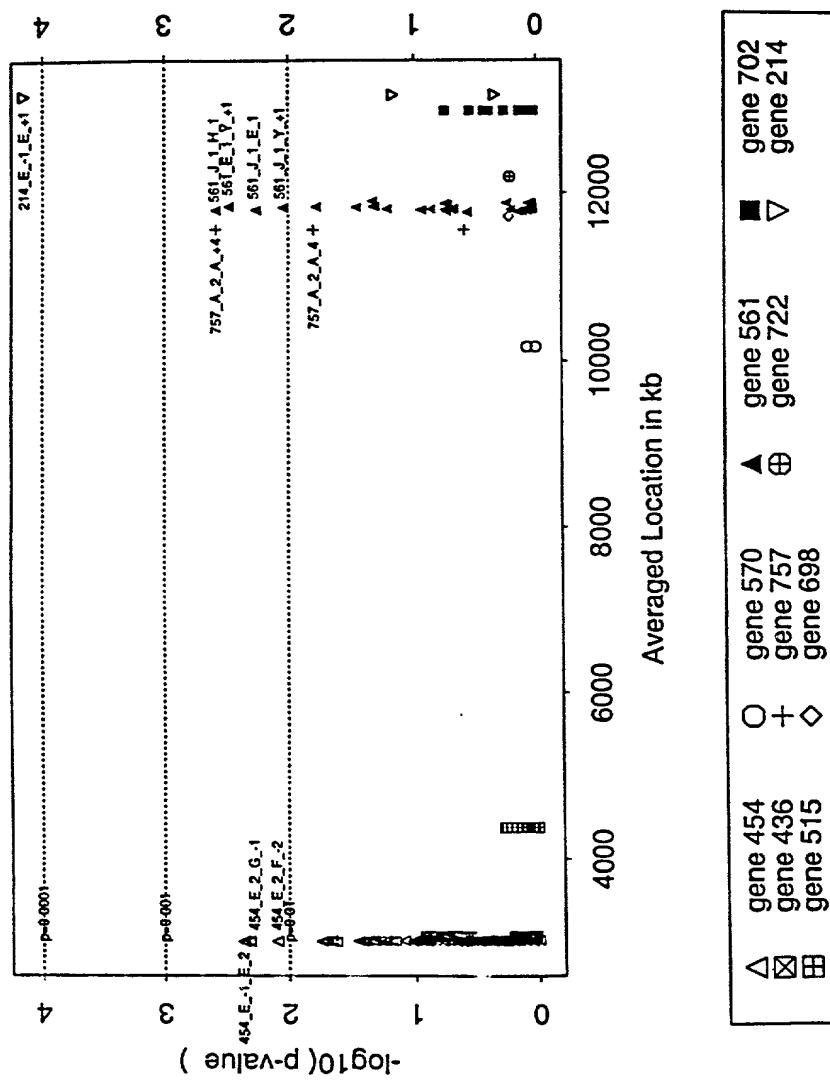


FIG. 21

Chr. 12 Case(BHR (PC₂₀ \leq 16 mg/ml) & Asthma)/Control: Haplotype

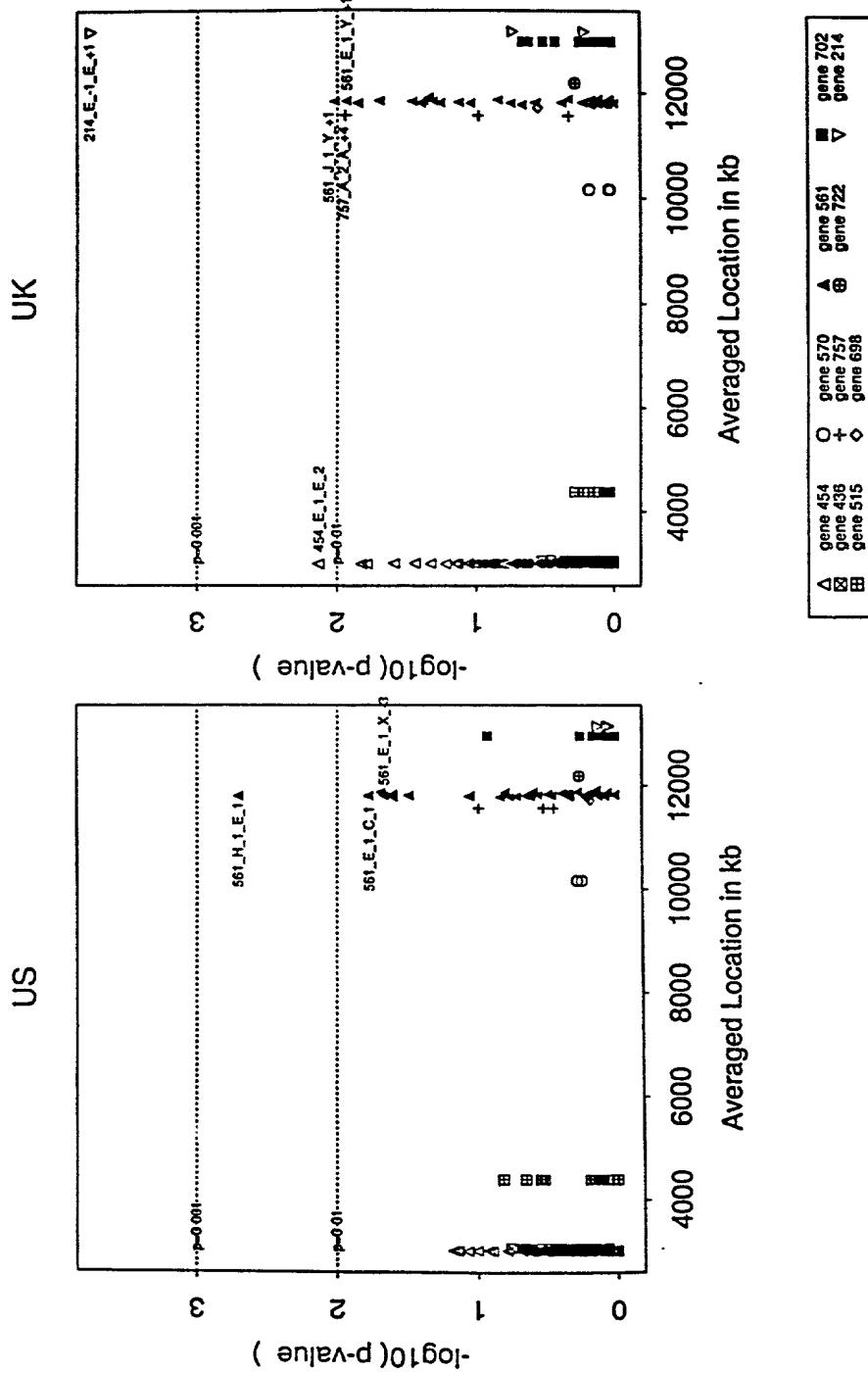


FIG. 22

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

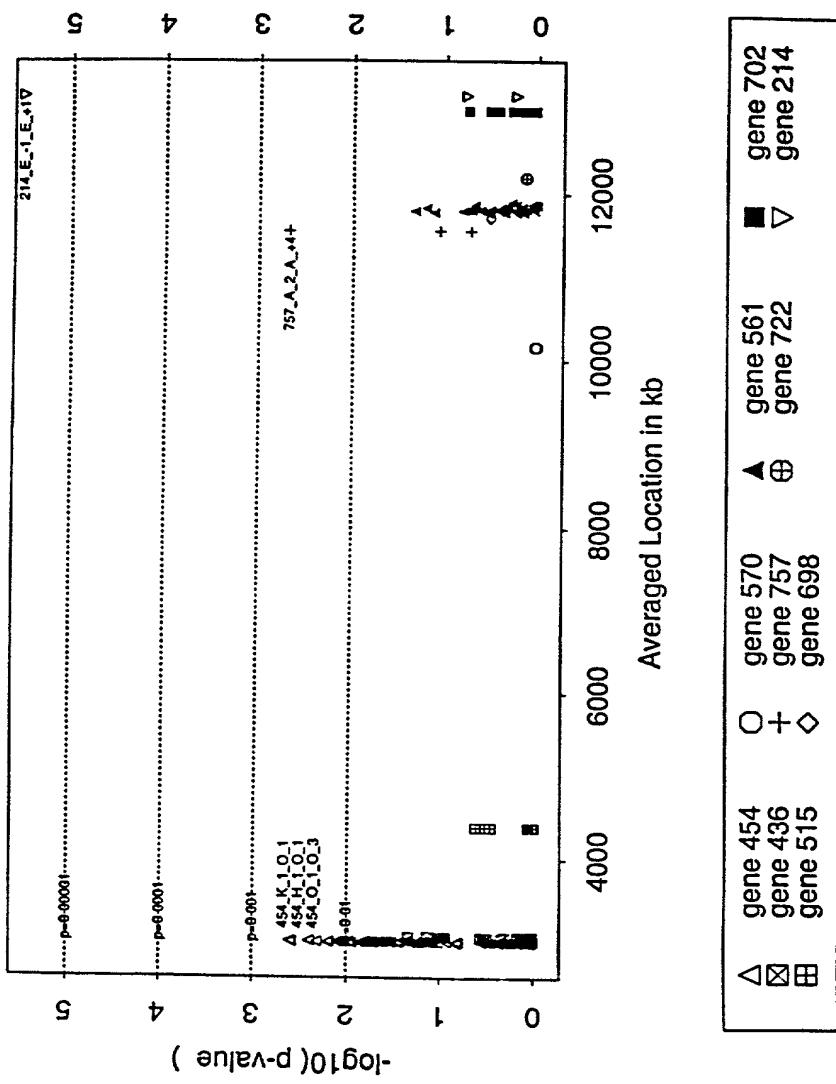


FIG. 23

Chr. 12 Case(Total IgE & Asthma)/Control: Haplotype

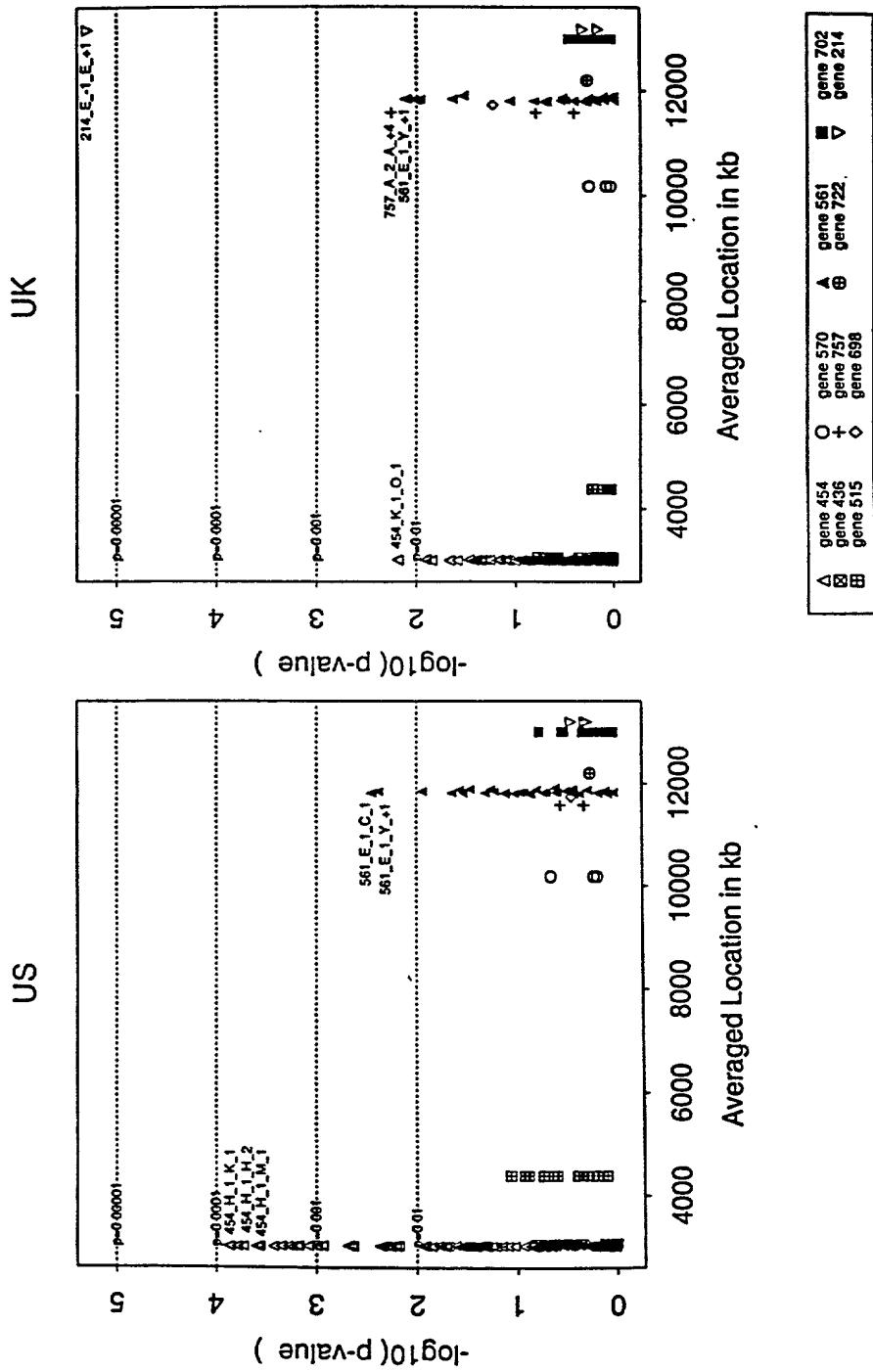


FIG. 24

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

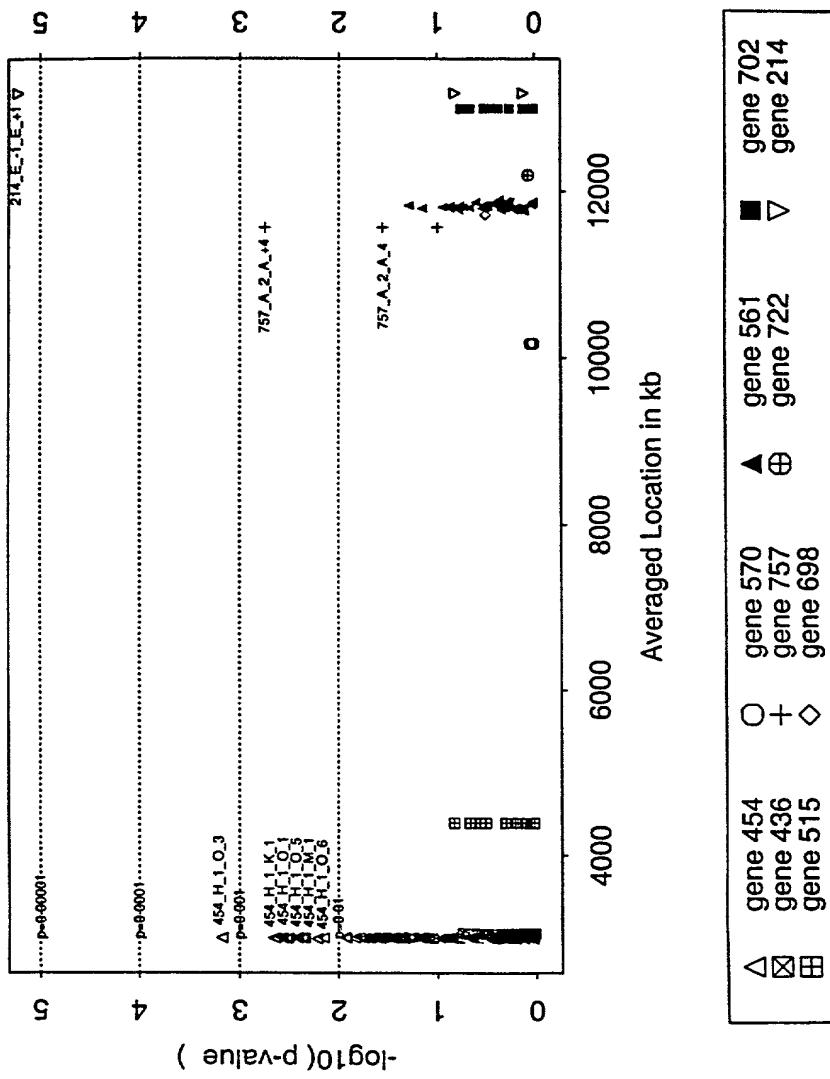


FIG. 25

Chr. 12 Case(Specific IgE & Asthma)/Control: Haplotype

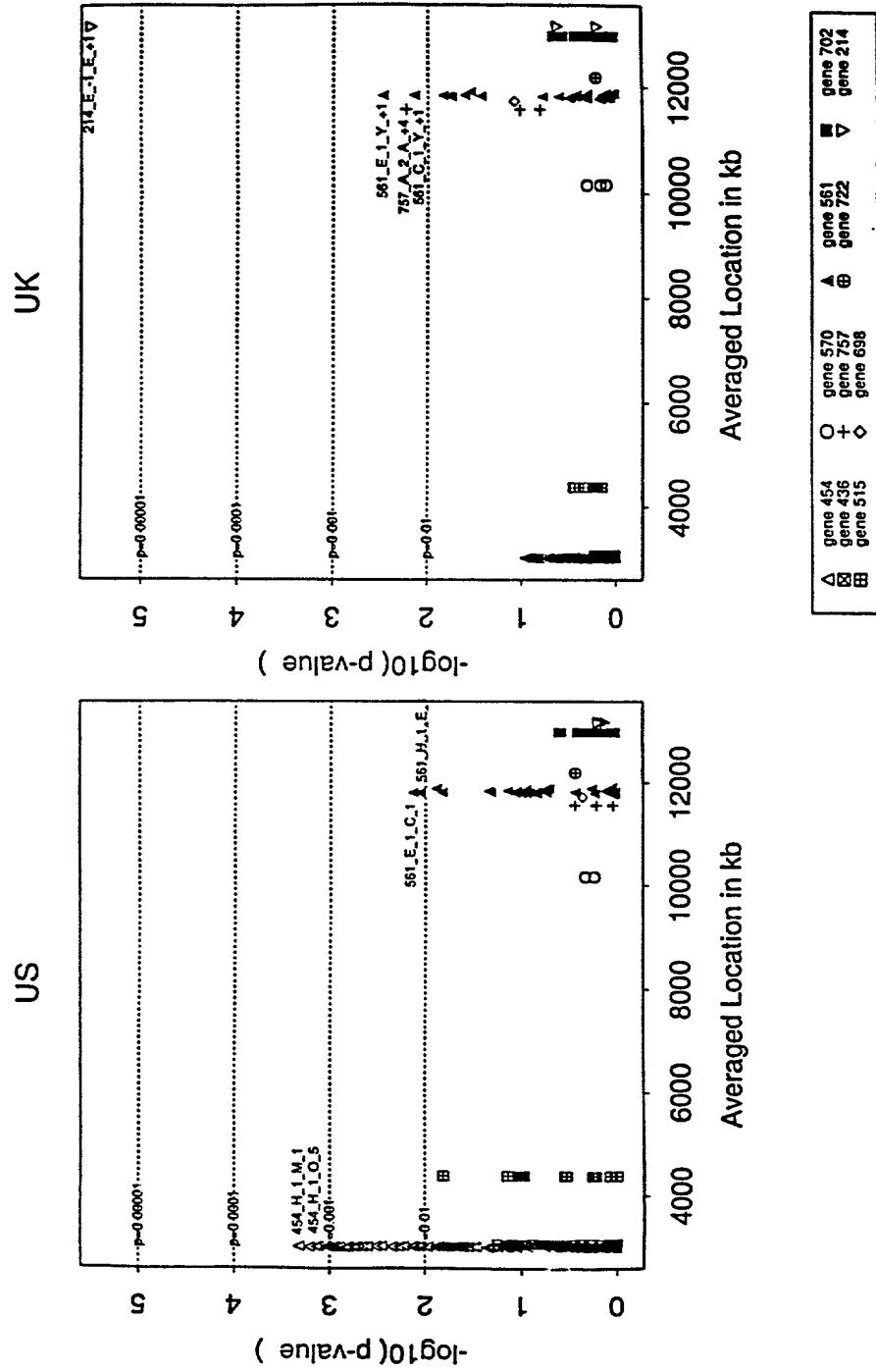


FIG. 26

10 30 50
CTTGGAAATGACCCGCCACACCTGAAGCCTGCAGGTGCTGAGGCCACATTGATCAGACC

70 90 110
CAAGCTTGGGAGACCGCTGGGAAATTCCCACTCCTCTCCTGAGACCAGGAACTCAG

130 150 170
CAGAGAAACTTGTGGAAATGAAC TGAAAGGATGCCACCCAGGGAGAGTATCTCCTGAGA

190 210 230
TCCCATCATGCAGGCCTTCCCACAAGGGCCCGCAGCATGACAAGGTGAAGGCAGAGTAT

250 270 290
GTGCATCTCAACCAYCCGCTCACCTCGTGACCAGAGAGCGCGATTGGCCGTGAAGGAG

310 330 350
AAACACCAGCTCCAAGCCAAGCTGGAGAACCTAGAACAGGTCTGAAGCATATGCCAGAG
MetArgGlu

370 390 410
GCGGCTGAACGGCGGCAGCAGCTGCAGTTGGAGCATGACCAGGCCCTGGCTGTTCTCAGT
AlaAlaGluArgArgGlnGlnLeuGlnLeuGluHisAspGlnAlaLeuAlaValLeuSer

430 450 470
GCCAAGCAGCAGGAAATTGACCTCTGCAGAAGTCCAAGGTTCGAGAGCTGGAAAGAGAAA
AlaLysGlnGlnGluIleAspLeuLeuGlnLysSerLysValArgGluLeuGluLys

490 510 530
TGCCGGACTCAAAGTGAGCAGTTCAACCTGCTGTCCCGGGACCTGGAGAAGTTCCGGCAG
CysArgThrGlnSerGluGlnPheAsnLeuLeuSerArgAspLeuGluLysPheArgGln

550 570 590
CACGCTGGCAAGATTGACCTGCTGGGTGGCAGCGCGGTGGCCCCCTGGACATCTCCACG
HisAlaGlyIleAspLeuLeuGlyGlySerAlaValAlaProLeuAspIleSerThr

FIG. 27 A

610 630 650
GCCCCCAGCAAGCCTTCCCACAGTTCATGAATGGCCTAGCCACCTCCCTGGCAAAGGT
AlaProSerLysProPheProGlnPheMetAsnGlyLeuAlaThrSerLeuGlyLysGly

670 690 710
CAGGAGAGCGCTATTGGAGGCAGCTCTGCGATCGGTGAATATATCCGGCCCTTCCGCAG
GlnGluSerAlaIleGlyGlySerSerAlaIleGlyGluTyrIleArgProLeuProGln

730 750 770
CCTGGTGACAGGCCGGAGCCTCTGTCCCGCCAAGCCCACCTCCTGTCGAGATCCGGTAGC
ProGlyAspArgProGluProLeuSerAlaLysProThrPheLeuSerArgSerGlySer

790 810 830
GCAAGATGCAGATCTGAGTCAGACATGGAGAATGAACGAATCCAATACTCCAAGCAG
AlaArgCysArgSerGluSerAspMetGluAsnGluArgAsnSerAsnThrSerLysGln

850 870 890
AGATACTCGGGGAAGGTCCACCTCTGTGTTGCCGCTATAGTTACAACCCCTCGATGGA
ArgTyrSerGlyLysValHisLeuCysValAlaArgTyrSerTyrAsnProPheAspGly

910 930 950
CCGAACGAGAACCCCGAACGCTGAGCTGCCCTCACGGCGGAAAATACCTCTACGTCTAT
ProAsnGluAsnProGluAlaGluLeuProLeuThrAlaGlyLysTyrLeuTyrValTyr

970 990 1010
GGAGACATGGATGAGGATGGGTTCTATGAAGGAGAGCTCCTCGATGCCAGAGGGGTCTG
GlyAspMetAspGluAspGlyPheTyrGluGlyGluLeuLeuAspGlyGlnArgGlyLeu

1030 1050 1070
GTGCCCTCCAACTTCGTGGACTTGTGCAGGACAACGAGTCCGCGGTTGGCAAGCAGCTG
ValProSerAsnPheValAspPheValGlnAspAsnGluSerArgLeuAlaSerThrLeu

1090 1110 1130
GGGAACGAGCAGGATCAGAACTTCATCAACCATTCCGGCATGGCCTGGAGGGAGAGCAC
GlyAsnGluGlnAspGlnAsnPheIleAsnHisSerGlyIleGlyLeuGluGlyGluHis

1150 1170 1190
ATCCTGGACCTCCACTCCCCAACCCACATAGATGCGGGATCACCGACAACAGTGCCGGG

FIG. 27 B

IleLeuAspLeuHisSerProThrHisIleAspAlaGlyIleThrAspAsnSerAlaGly

1210

1230

1250

ACCCCTGGACGTGAACATCGACGACATCGGAGAAGACATCGTGCCTTACCCCTAGAAAAATC
ThrLeuAspValAsnIleAspAspIleGlyGluAspIleValProTyrProArgLysIle

1270

1290

1310

ACCCCTCATCAAACAACACTGCCAAAAGTGTATTGTGGGCTGGGAGCCCCGGCGGTGCCA
ThrLeuIleLysGlnLeuAlaLysSerValIleValGlyTrpGluProProAlaValPro

1330

1350

1370

CCAGGATGGGAAACGGTGAGCAGCTACAACGTCTGGTGACAAGGAGACACGCATGAAC
ProGlyTrpGlyThrValSerSerTyrAsnValLeuValAspLysGluThrArgMetAsn

1390

1410

1430

CTCACGCTGGGAGCAGAACTAAAGCCCTCATCGAGAACGCTAACATGGCAGCCTGCACC
LeuThrLeuGlySerArgThrLysAlaLeuIleGluLysLeuAsnMetAlaAlaCysThr

1450

1470

1490

TACCGCATCTCCGTGCAGTGCCTCACAGCAGGGCAGCTCGGATGAGCTGCAGTCACG
TyrArgIleSerValGlnCysValThrSerArgGlySerSerAspGluLeuGlnCysThr

1510

1530

1550

CTGCTGGTGGCAAGGACGTGGTGGTGGCCCTCCCACCTGCGGGTGGACAACATCAGC
LeuLeuValGlyLysAspValValAlaProSerHisLeuArgValAspAsnIleThr

1570

1590

1610

CAGATCTCCGCCAGCTCCCTGGCTACCCACCAACAGCAACTACAGCCACGTCACTTC
GlnIleSerAlaGlnLeuSerTrpLeuProThrAsnSerAsnTyrSerHisValIlePhe

1630

1650

1670

CTCAACGAGGAGGAGTTGACATCGTCAAGGCCAGGTACAAGTACCAAGTCTTCAAT
LeuAsnGluGluGluPheAspIleValLysAlaAlaArgTyrLysTyrGlnPhePheAsn

1690

1710

1730

CTCAGGCCAACATGGCTATAAGGTGAAGGTTCTGGCAAACCCCACCAAGATGCCGTGG
LeuArgProAsnMetAlaTyrLysValLysValLeuAlaLysProHisGlnMetProTrp

FIG. 27 C

1750 1770 1790
 CAGCTCCGCTGGAGCAAAGGGAGAAGAAGGAGGCCTTGTGGAGTTCTCCACGTTGCCT
 GlnLeuProLeuGluGlnArgGluLysLysGluAlaPheValGluPheSerThrLeuPro

1810 1830 1850
 GCAGGACCCCCCAGCACCCCCACAAGATGTTACCGTCCAGGCTGGGGTGACCCCCGCCACC
 AlaGlyProProAlaProProGlnAspValThrValGlnAlaGlyValThrProAlaThr

1870 1890 1910
 ATCCGGGTCTCCTGGAGACCACCTGTGCTGACGCCAACCGGGCTGTCCAATGGCGCAAAC
 IleArgValSerTrpArgProProValLeuThrProThrGlyLeuSerAsnGlyAlaAsn

1930 1950 1970
 GTTACCGGCTACGGCGTGTATGCCAAAGGGCAGAGGGTGGCTGAAGTCATCTCCCCACG
 ValThrGlyTyrGlyValTyrAlaLysGlyGlnArgValAlaGluValIlePheProThr

1990 2010 2030
 GCAGACAGCACGGCGTGGAGCTTGTGCGGCTGCGGAGCCTGGAGGCCAAGGGCGTGACC
 AlaAspSerThrAlaValGluLeuValArgLeuArgSerLeuGluAlaLysGlyValThr

2050 2070 2090
 GTGCGGACCCCTCTCCGCCCAAGGGCGAGTCCCGTGGACTCTGCAGTTGCTGCCGTTCCCCC
 ValArgThrLeuSerAlaGlnGlyGluSerValAspSerAlaValAlaAlaValProPro

2110 2130 2150
 GAGCTCCTGGTGCCTCCTACCCCCCACCGAGACCTGCACCCCAATCAAAGCCATTAGCA
 GluLeuLeuValProProThrProHisProArgProAlaProGlnSerLysProLeuAla

2170 2190 2210
 AGTTCTGGAGTCCCCGAAACCAAAGACGAGCAGCACCTGGGTCCCCACGCCAGGATGGATGAG
 SerSerGlyValProGluThrLysAspGluHisLeuGlyProHisAlaArgMetAspGlu

2230 2250 2270
 GCCTGGGAGCAGAGCCGTGCACCTGGCCCTGTGCATGGGCACATGCTGGAGGCCCGCGTG
 AlaTrpGluGlnSerArgAlaProGlyProValHisGlyHisMetLeuGluProProVal

2290 2310 2330
 GGCCCCCGGAAGGCGGTGCCCTCACCCAGCCGCATCCTGCCGCAGCCACAGGGCACCCCG

FIG. 27 D

GlyProGlyArgArgSerProSerProSerArgIleLeuProGlnProGlnGlyThrPro

2350

2370

2390

GTGTCCACCACCGTCGCCAAGGCCATGGCCGGAGGCCGCAGAGGGTGGCCGAGAGC
ValSerThrThrValAlaLysAlaMetAlaArgGluAlaAlaGlnArgValAlaGluSer

2410

2430

2450

AGCAGGTTAGAGAAAAGGAGCGTCTCCTAGAGAGAACGAGCGGGGGCAGTACGCCGC
SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla

2470

2490

2510

TCAGACGAGGAGGACGCCATTGACTCTCCAGACTTCAAGAGGAGGGGCGCCTCGGTGGAC
SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp

2530

2550

2570

GACTTCCTGAAAGGCTCTGAACCTGGCAAGCAGCCGCACTGTTGCCATGGAGACGAGTAC
AspPheLeuLysGlySerGluLeuGlyLysGlnProHisCysCysHisGlyAspGluTyr

2590

2610

2630

CACACAGAGAGCAGCCGGGGTCTGACCTCTCAGACATCATGGAGGAGGACGAGGAGGAG
HisThrGluSerSerArgGlySerAspLeuSerAspIleMetGluGluAspGluGlu

2650

2670

2690

CTGTATTCTGAAATGCAGCTGGAAAGATGGGGGAAGGAGGCGGCCAGCGGCACGTCCCCAC
LeuTyrSerGluMetGlnLeuGluAspGlyGlyArgArgProSerGlyThrSerHis

2710

2730

2750

AATGCCCTCAAGATTTAGGAACCCAGCCTCTGCAGGACGGGTGGATCACATGGCCGG
AsnAlaLeuLysIleLeuGlyAsnProAlaSerAlaGlyArgValAspHisMetGlyArg

2770

2790

2810

AGGTTTCCCCGTGGCAGCGCTGGTCTCAGAGGTCCCAGCCGTGACAGTCCCACATCCATC
ArgPheProArgGlySerAlaGlyProGlnArgSerArgProValThrValProSerIle

2830

2850

2870

GACGATTACGGCGAGACCGCCTTCTCCAGACTTCTATGAAGAGTCAGAAACTGACCCCT
AspAspTyrGlyArgAspArgLeuSerProAspPheTyrGluGluSerGluThrAspPro

FIG. 27 E

TOP STRAND

2890 2910 2930
GGTGCCGAAGAGCTCCGGCCGGATCTTGCTCTTGACTACGACCCGCTCACC
GlyAlaGluGluLeuProAlaArgIlePheValAlaLeuPheAspTyrAspProLeuThr

2950 2970 2990
ATGTCCCCAACCCAGATGCTGCAGAGGAGGAGCTTCCCTTAAAGAAGGCCAGATCATC
MetSerProAsnProAspAlaAlaGluGluLeuProPheLysGluGlyGlnIleIle

3010 3030 3050
AAGGTTATGGTATAAGACGCTGATGGATTCTACCGTGGGAAACCTGTGCCCGGCTT
LysValTyrGlyAspLysAspAlaAspGlyPheTyrArgGlyGluThrCysAlaArgLeu

3070 3090 3110
GGCCTTATTCTTGTAACATGGTCTCTGAGATACAAGCAGATGATGAGGAGATGATGGAT
GlyLeuIleProCysAsnMetValSerGluIleGlnAlaAspAspGluGluMetMetAsp

3130 3150 3170
CAGCTTCTTAGACAGGGCTTCTCCCTCTGAATACACCTGTGGAGAAAATAGAGAGAAC
GlnLeuLeuArgGlnGlyPheLeuProLeuAsnThrProValGluLysIleGluArgSer

3190 3210 3230
AGGAGAAAGTGGCAGGCGTCATCGGTATCGACGCGGAGAATGGTGGCCCTGTATGACTAC
ArgArgSerGlyArgArgHisSerValSerThrArgArgMetValAlaLeuTyrAspTyr

3250 3270 3290
GACCCCAGAGAAAGCTGCCCAACGTCGATGTCGAGGCCGAACCTACATTTGCACAGGA
AspProArgGluSerSerProAsnValAspValGluAlaGluLeuThrPheCysThrGly

3310 3330 3350
GATATTATTACAGTTTGGTCAAATTGATGAAGATGGATTTATTATGGGGAGCTGAAC
AspIleIleThrValPheGlyGluIleAspGluAspGlyPheTyrTyrGlyGluLeuAsn

3370 3390 3410
GGGCAGAAAGCCTGTGCCCTCAAACCTTGGAAAGAAGTGCCTGATGACGTAGAAC
GlyGlnLysGlyLeuValProSerAsnPheLeuGluValProAspAspValGluVal

3430 3450 3470
TATCTTCTGATGCTCCATCCCACTACTCTCAAGATAGCCAATGCGCTCAAAGGCAAAA

FIG. 27 F

TyrLeuSerAspAlaProSerHisTyrSerGlnAspThrProMetArgSerLysAlaLys

3490

3510

3530

AGGAAGAAGAGTGTTCATTCATACTTAATCAGGCAATGTAGCCTCACGTAAGTGAGC
ArgLysLysSerValHisPheIleProEnd

3550

3570

3590

AACTGAAGATAACGATAAAGATAACCAACTTAAGCTACCTAACCGGGCCAGTGTGGTAGA

3610

3630

3650

CTTAAGGCTTCATTGTGGGTTAAAAAAAAAAAAAGATAAAAGAAATATGTCTCAAAA

3670

3690

3710

ACTATTGGACCTAAATAATTAGAATATTACTTGGTCTCAGTTGTAAGCAACTGAATTAA

3730

3750

3770

TAGTGAAGCAAATCATCTTAATAATCATTTCTACTATTGCATTAAGAATATTTGAAA

3790

3810

3830

GGCCAACATTGGAACATATTCTTAACAAGCTAACTGTGTGTTACATAGAGAGAGCTG

3850

3870

3890

CATATTGCATTGTTAGCCACTCTTGGAAAAGCACAACCTAACAAACATGTTACTATAG

3910

3930

3950

GAAGCTTTACTTAGAAACTTAACCCAAGGTCAAGCAGATGAGTAGTGAACACAGGTGAT

3970

3990

4010

CGAGTGTGGCTCTGAACACTCCAAACACTGGCTCGAGTGGCCAGAACGTGTTCTTA

4030

4050

4070

AGTAACCCTGCCTCTACCTTACGAGAGAGCTATGCTCCTCTCAAAGCACAATCATCCTG

4090

4110

4130

TGACAGAAGTTGCTGCAACACGCGTTGTTGGTATACCAATGCAATACTAAGTTGAT

FIG. 27 G

TOEPLITZ SEQUENCER

4150 4170 4190
GAAGCACGCAGCTCAAATGATCACATTAGATGGAATAGATGGTATCTCAGGTGTACTTT

4210 4230 4250
GGGATGCTTTACTAGGTGTTTCCATTAGAATTAGACCTTGATTTAAATCCAAGCAAGC

4270 4290 4310
TTGAAGCCCCTGGCTTACAGCATTGCCTGCTGAATACTAACACTCACATGGCAAGAG

4330 4350 4370
TTGCTCTGGAGAGGTAGGCCAGAGGAATGCTGCTGCAGCGTACTGCCACTCAGGCACATGCTT

4390 4410 4430
AGCTGTAAAGGGAAAGCGAGGTGAAGTCGTCTGCAGCGTATTAGAGTAAAAGTCTACCCC

4450 4470 4490
TCTGAAGCACTATTAAGCGTTAACGTATATTAAATACTACCATGTGCTATCTACTGAG

4510 4530 4550
GAAGATTCAATTAGGAAATAATGCAAGCATTCAAGGGCTTAAGCTT

4570 4590 4610
TCTTGATTATAATTAGGTTCAATTAGGTTCTTCTTCTTCAACCAGTGTGCCAT

4630 4650 4670
CTCCAATATTCTATAGTATACCAACCACCCAGGAATGCACCTAACAAATATCAGGATT

4690 4710 4730
TTATATAACCAAATAGTTCAAATACAACAAAATTCCCTTATGAACCTTCGCTTTAA

4750 4770 4790
GACTACTGATGGGTACTCGGCCAACCTTACTATCAACCTAACAGATCATGTCTCCCC

FIG. 27 H

4810 4830 4850
TGCCCTTAGTCTTCATTATGAAGTGAATTATTACCTGCCTTAGCTTGCCAAAGCAACG

4870 4890 4910
GCCACCCCCGCACTCCCTCGAGACAGAGAAACGGAACCCACACATTTATGTCTGGGCCTC

4930 4950 4970
TCTCTGGCGTGTGGAGAGGACCTTGCTTCTCATGGCATACTCAACAACGTGAAAG

4990 5010 5030
AACAAATGAACCCCCCTGACCTTCCTGGTGGAAACGGGACAGTACGATGTTACCAAG

5050 5070 5090
TGAATTCTGTGTGGCGCTCACACACTCAATAAACTGTAACACTGTACCTACTAGGTT

5110 5130 5150
CTCCTGAGGGTTCAGGTACAGCAAGGAGAGCTCCATCCCCACAGTCCATCTCCATTGG

5170 5190 5210
GGTCACCTACGTCATCTATGGTTCTGGTAGTCCTGGAGAGGCAGGGAAATGTCCTCGA

5230 5250 5270
AAAAGAAAAAGGGCTGTTCAAAGGCAAGAAAATGCTGAAAAAGCTGGTGCAGTGA

5290 5310 5330
AATGATTCATGTGCTTCCGGACAAC TGCCAAATCTATGTAATTTCTTAATTCAAAC

5350 5370 5390
AGGGCTTCATGACTCAAGTACTCCTAAAAAACCAATCTCTCCCCTGACACCAAGTA

5410 5430 5450
GAGAAATGCACTTGCACTACCAACCACTTAACCAACCACGAGAACAAAGAGGAGCG

5470 5490 5510

GTTGCTCTGTCAACCGCTGGCAGTCTGCTCTCATTGTCCAAGCTCTGATTTGGGAGGTG

5530 5550 5570
GGAGGGGACGTCTTATTAACAAACGGGGGCAGCATAGCTATCACCTGTAGCTCCCTCCCTA

5590 5610 5630
CCTGTAATTCCAGTCTTGTGCATTGTCATCTGCCCTAAAGGAATGATTTAACCTT

5650 5670 5690
TCTCCCTCTCAAAATGCTGCCTCATAATGCATAACTTCACACTTGACTCTGGTCTTGA

5710 5730 5750
AATTCCCTAGTTAATTGCCCTGATGTTCTGCCCTATAAAATGCACAATGATTTGACTGT

5770 5790 5810
CTAATAAAAACAGTGTATACTTGTATGTGTCGTGCATTCACTGGTCTTCATCCTGACAC

5830 5850 5870
AGTGGTTCGAGATCAAGTTGTACAGGCTGTGCATTTAAGATACTAGTTCACTTTCA

5890 5910 5930
AAGCCAGCCAGGCTACACACAGAAAATGTTACTCAATCATTCAAAAAAGAGAAAAGGAG

5950 5970 5990
AGAAAAGTAACTTGTTGGTAAAGCACCAGTACTCCAACCTTCCAGAAAGCCGATTATCT

6010 6030 6050
TCATTGCTTTAATGTTCTATTCTGTGGCATATGGTTCTGTTACTTCGTGTCAAAA

6070 6090 6110
TGCCATACCCAAATACACAGCAATGAATGGCACACAAGTAATCCACATAATGCATAAGCC

6130 6150 6170
ACACCAAAACCACTCAATTAAATCTGCTCCAAATGAGTCCATACCCATCTTCATCAT

6190 6210 6230
TGGCATTGAAACAAAAGACTTACTTACAAAGTTGCTGGCAGATGTATTTGATGGTTACTC

6250 6270 6290
TTTGTAATTCTTGTCCACTGTAAATTGTTTACTCTTATACATACTTTCAGACTG

6310 6330 6350
CCTTCCTTTGTAATTATGGACGGTTATAAATGAATGACAAAGCTTCCCCATTGTGT

6370 6390 6410
CTTCAAAAACGCTATTATAAATTGTAATATAATAGTATGTGGTAGATTATTAAAGG

6430 6450 6470
AAATCCATGTGTGGTTAAGCTCTGTGTGGGTGTGCATGTGCACAGTTAGTGTAAAATA

6490
TTTCTAGAAATAAAATTGTTATTTAT

FIG. 27 K

10	30	50
GGTCCCCACGCCAGGATGGATGAGGCCTGGGAGCAGAACCTGTGCACCTGGCCCTGTGC MetAspGluAlaTrpGluGlnLysProValHisLeuAlaLeuCys		
70	90	110
ATGGGCACATGCTGGAGCCGCCGTGGCCCCGCATCCTGCCACAGCCACAGGGCACCCC MetGlyThrCysTrpSerArgProTrpAlaProHisProAla <u>ThrAlaThrGlyHisPro</u>		
130	150	170
GGTGTCCACCACCGTCGCCAAGGCCATGGCCGGGAGGCCGCAGAGGGTGGCGAGAGC GlyValHisHisArgArgGlnGlyHisGlyProGlyGlyArgAlaGluGlyGlyGluSer		
190	210	230
AGCAGGTTAGAGAAAAGGAGCGTCTCCTAGAGAGAACGAGCAGCGCGGGCAGTACGCCGCC SerArgLeuGluLysArgSerValPheLeuGluArgSerSerAlaGlyGlnTyrAlaAla		
250	270	290
TCAGACGAGGAGGACGCCATTGACTCTCCAGACTTCAAGAGGAGGGCGCCTCGGTGGAC SerAspGluGluAspAlaTyrAspSerProAspPheLysArgArgGlyAlaSerValAsp		
310	330	350
GACTTCCTGAAAGGCTCTGAACCTGGCAAGCAGGGAAACTGAGGCCACAGAATTGAGAA AspPheLeuLysGlySerGluLeuGlyLysGlnGlyAsnEnd		
370	390	410
TTTTGTCCATGATTACGCAGATGGCTCCTAACAGAGCTGGAATTAGATTGAACCGAGG		
430	450	470
CCTGAAGAAGACCTGTTCCACGCCCTTCCCATGTGCCACGTTCTCCTCACCTATCCAG		
490	510	530
GAGTGAATCATCACCTCCCTGCAATCTGCTCAGGTTACAAACCCGGAGGAAAGGCTGGA		
550	570	590
GCACTTGTTCTCTGGGTGAAGGACCCATACCCCCACTGGTTTGAGATCGGCATTCA		

FIG. 28 A

610 630 650
GCTGTCTTATGGCAGCCMCAGCCCCAGGTGGCCCCAGAGCCCTTGACATGTGGCACCTG

670 690 710
GGGCTGAGTGTGACTGAGGCCCTGAATTTACTTCTATAAAATTAGTTCCAGATTAGTT

730 750 770
TACATTCTAATTAGTTACATGTAAACAGCCACACGTGGCTGGTGGCCACCAGTGCTGA

790 810 830
CGCCCAGCTCTGGATGACCACACCTGCTACAAGAGATGACTTTCTAGAGAAGAGTAGAA

850 870 890
ACACAGCGGCAGAAACACAGCTCTGCACTCCGAGGGCCTCCACTCCTCTGATGAGAC

910 930 950
TGCAGAGGAAGTCTGTTGCCAACGATGCTTAACACGTTTCCTGTTGTTGTT

970 990 1010
TTAACAGAGCAAACAGGTCTGTTCTATTAAAAATTAAAAAGCGTTAATATTARCAGC

1030 1050 1070
ATTGTTTATGTTGATTCAACATAATAACATAACATATTGTTAATATATA

1090 1110 1130
TTGTTAATAATATAATAACATAAAAAGTGTAAATATTGATTCAATTCAAAGAATACATTAA

1150 1170 1190
AGATATTCTTAAAAGTAACGTTAAATATTGATTCAATTCAAAGAATACATTAA

1210 1230 1250
TCATACAGATGGCGTCTGGCTAGGTGACGCATCATGACAGTGGTAGGGAGTGACTGAAGT

1270 1290 1310

FIG. 28 B

TGAGCTGGTGCACAGACTGCCAGTTACAACCCGGGAAGTGTCCCTGACCATCCGCTT

1330

1350

1370

CCCCATGCTGCCCGCCCCGTCACATGAGCCCTTACCCCTGGCGTATCCCATCTGCTCC

1390

1410

1430

AAGACACCGATGTTCTAGTGGGTGGAAGCCTCCACTTTAGTTGACTACGGTATCTCTAG

1450

1470

1490

CATTTCACACATAGTAGGTGCTCAATGAATGTTGTCGAATGAATGAAAGAAGGGA

1510

1530

1550

GGCTGAGAGTAGCTGGGACATTCGCTCTGAAAAAATCACCTCCATTCTCCAATATTACA

1570

1590

1610

AAAGCATTTCATTAAGTCCACAATGAAAAATGCTCACTGTACCAATAATAATATCTT

1630

1650

AGTTATCTATTTAAAAGTAAAAAAAAACCTCGTGCCGAAGTC

FIG. 28 C